

SEQ ID	Model	Description	E-value	Score	Repeats	Position
						344:345-374:375-407
1701	URO-D	Uroporphyrinogen decarboxylase (URO-D)	7.8	-229.7	1	79-354
1702	pkina	Protein kinase domain	0.00012	-68.0	1	31-278
1702	HEAT	HEAT repeat	1.2	15.6	2	342-380:499-537
1705	cyclin	Cyclin, N-terminal domain	3.8e-11	50.5	1	157-279
1708	WD40	WD domain, G-beta repeat	1.5e-11	51.8	5	278-313:371-407:413-447:493-529:535-569
1709	SH2	SH2 domain	0.002	10.0	1	287-364
1710	abhydrolase	alpha/beta hydrolase fold	2.2e-20	81.2	1	124-355
1710	abhydrolase 2	Phospholipase/Carboxylesterase	1.2	-84.9	1	179-359
1711	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	0.002	23.7	1	280-320
1711	PHD	PHD-finger	1.9	-12.4	1	282-323
1712	WD40	WD domain, G-beta repeat	3.2e-18	74.0	5	67-101:123-157:164-199:209-246:253-290
1714	Acyltransferase	Acyltransferase	0.0011	14.0	1	83-217
1719	helicase_C	Helicase conserved C-terminal domain	1.2e-19	78.7	1	397-475
1719	DEAD	DEAD/DEAH box helicase	4.6e-07	10.4	1	2-210
1719	IPT	Isopentenyl transferase	7.9	-160.7	1	17-172
1720	Na_Ca_Ex	Sodium/calcium exchanger protein	8e-76	265.3	2	109-249:471-616
1720	DUF205	Domain of unknown function DUF	5.3	-112.7	1	85-253
1720	Fumarate_red_D	Fumarate reductase subunit D	8.4	-49.5	1	518-620
1721	vwa	von Willebrand factor type A domain	9.6e-29	108.9	1	34-205
1721	fn3	Fibronectin type III domain	3e-15	64.1	2	212-287:332-413
1724	pkina	Protein kinase domain	1.6e-06	-41.3	1	40-359
1725	BRCT	BRCA1 C Terminus (BRCT) domain	1e-15	65.6	3	3-93:642-730:753-833
1727	BRCT	BRCA1 C Terminus (BRCT) domain	7.2	1.2	1	45-130
1728	rrm	RNA recognition motif	1.1e-05	32.4	2	545-612:880-942
1728	zf-CCCH	Zinc finger C-x8-C-x5-C-x3-H type	0.012	22.2	1	285-311
1728	PWI	PWI domain	0.047	-0.6	1	6-78
1730	PX	PX domain	2.5e-31	117.5	1	94-211
1731	PMP22_Claudin	PMP-22/EMP/MP20/Claudin family	1.5e-56	201.3	1	1-157

SEQ ID	Model	Description	E-value	Score	Repeats	Position
1733	homeobox	Homeobox domain	0.00037	21.6	1	268-339
1733	Vac_Fusion	Chordopoxvirus fusion protein	5.2	-21.5	1	286-364
1733	CUT	CUT domain	8.5	-38.0	1	159-240
1734	homeobox	Homeobox domain	0.00037	21.6	1	268-339
1734	Vac_Fusion	Chordopoxvirus fusion protein	5.2	-21.5	1	286-364
1734	CUT	CUT domain	8.5	-38.0	1	159-240
1738	efhand	EF hand	1.5e-16	68.4	2	40-68;76-104
1742	trypsin	Trypsin	6.5	-55.6	1	33-255
1743	Exonuclease	Exonuclease	1.2e-36	135.2	1	39-213
1745	Smr	Smr domain	0.0029	13.0	1	1594-1672
1745	RyR	RyR domain	1.5	-29.0	1	1312-1403
1745	L27	L27 domain	3.6	5.1	1	1573-1626
1746	Smr	Smr domain	0.0029	13.0	1	1611-1689
1746	RyR	RyR domain	1.5	-29.0	1	1312-1403
1746	L27	L27 domain	3.6	5.1	1	1590-1643
1746	Smg4_UPF3	Smg-4/UPF3 family	9.7	-74.5	1	1379-1518
1747	mito_carr	Mitochondrial carrier protein	1.3e-81	284.5	3	1-90;98-198;200-288
1748	OSCP	ATP synthase delta (OSCP) subunit	8.4	-94.4	1	67-213
1749	Oxysterol BP	Oxysterol-binding protein	3.4e-78	273.2	1	488-875
1749	PH	PH domain	2.2e-09	44.6	1	52-146
1750	lactamase B	Metallo-beta-lactamase superfamily	4.1	-28.9	1	1-153
1751	lipoxxygenase	Lipoxygenase	9.5e-133	454.4	1	126-703
1751	PLAT	PLAT/LH2 domain	1.6e-33	124.8	1	2-116
1753	Rho_GDI	RHO protein GDP dissociation inhibitor	3.2e-113	389.5	1	1-187
1756	GRAM	GRAM domain	7.5e-17	69.4	1	110-177
1757	homeobox	Homeobox domain	3.6e-29	110.3	1	21-77
1758	lipocalin	Lipocalin / cytosolic fatty-acid binding pr	1.1e-24	95.4	1	38-168
1759	ig	Immunoglobulin domain	3.1e-13	57.4	2	35-112;160-234
1761	oxidored_q1	NADH-Ubiquinone/plastoquinone (complex I)	0.078	-128.7	1	16-259
1761	DUF250	Domain of unknown function, DUF250	0.45	-85.1	1	162-337
1761	DUF6	Integral membrane protein DUF6	2.5	-14.8	1	192-328
1761	secY	eubacterial secY protein	7.2	-246.6	1	36-243
1761	FecCD	FecCD transport family	9.8	-221.2	1	120-328
1762	Keratin_B2	Keratin, high sulfur B2 protein	3.3e-07	32.9	2	11-113;114-204
1763	sugar_tr	Sugar (and other) transporter	0.018	-119.2	1	43-449
1763	oxidored_q1	NADH-Ubiquinone/plastoquinone (complex I)	4.7	-165.1	1	146-442
1765	VPS9	Vacuolar sorting protein 9 (VPS9) domain	4.5e-33	123.3	1	380-484
1765	RA	Ras association (RalGDS/AF-6) domain	0.73	-5.9	1	518-607

SEQ ID	Model	Description	E-value	Score	Repeats	Position
1766	SSF	Sodium:solute symporter family	5.9e-206	697.6	1	106-535
1766	oxidored_q1	NADH-Ubiquinone/plastoquinone (complex I)	4.8	-165.2	1	216-521
1766	MIP	Major intrinsic protein	5.8	-121.9	1	112-364
1766	DsbD	Cytochrome C biogenesis protein transmembr	8.6	-97.3	1	195-425
1767	Peptidase_M3	Peptidase family M3	1.3e-203	689.8	1	251-701
1768	RasGAP	GTPase-activator protein for Ras-like	1.3e-26	101.9	1	449-621
1768	PH	PH domain	0.012	22.2	1	112-236
1768	C2	C2 domain	2.6	-10.9	1	249-332
1768	Tymo. 45 kd 70kd	Tymovirus 45/70Kd protein	4.2	-293.9	1	561-979
1768	RNA_pol	DNA-dependent RNA polymerase	5.1	-234.7	1	381-1225
1768	PHD	PHD-finger	6.9	-17.6	1	214-273
1770	rrm	RNA recognition motif	0.48	5.6	2	238-323:352-422
1772	zf-C2H2	Zinc finger, C2H2 type	1.6e-87	304.2	13	49-71:197-219:225-247:253-275:281-303:309-331:337-359:365-387:393-415:421-443:449-471:477-499:505-527
1772	zf-BED	BED zinc finger	8.9	-6.9	1	490-528
1773	ATP-synt_C	ATP synthase subunit C	5.4e-08	40.0	1	62-127
1774	zf-B_box	B-box zinc finger	7.2e-14	59.5	1	90-131
1774	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	1.6e-10	48.4	1	15-58
1774	PHD	PHD-finger	1.1	-10.3	1	14-61
1774	zf-AN1	AN1-like Zinc finger	1.4	-3.2	1	15-53
1774	zf-UBR1	Putative zinc finger in N-recoglin	7.6	-23.6	1	93-146
1775	FH2	Formin Homology 2 Domain	5.4e-50	179.5	1	21-455
1775	WH2	WH2 motif	0.0058	23.3	1	441-456
1777	PHD	PHD-finger	8.7	-18.6	1	493-522
1779	Branch	Core-2/1-Branching enzyme	3.9e-05	-52.8	1	175-516
1780	TFIIIS	Transcription factor S-II (TFIIIS)	3.9	-3.7	1	295-344
1781	SH3	SH3 domain	1.3e-13	58.6	1	454-508
1782	filament	Intermediate filament protein	3.9	-200.0	1	134-406
1783	SET	SET domain	2e-53	190.9	1	3878-4006
1783	PHD	PHD-finger	4.7e-28	106.6	3	20-71:72-118:147-200
1783	HMG_bo x	HMG (high mobility group) box	0.0047	12.3	1	710-773
1783	DC1	DC1 domain	8.5	1.7	3	19-50:69-98:146-176
1784	zf-DHHC	DHHC zinc finger domain	2.4e-25	97.7	1	90-154
1785	zf-C2H2	Zinc finger, C2H2 type	9.3e-14	59.1	4	18-40:64-86:92-

SEQ ID	Model	Description	E-value	Score	Repeats	Position
						115:178-200
1788	ion_trans	Ion transport protein	8.3e-18	72.6	1	438-672
1788	ank	Ankyrin repeat	1.9e-06	34.8	2	77-108:163-195
1788	Srg	C.elegans Srg family integral membrane prot	8.1	-222.4	1	418-669
1791	ubiquitin	Ubiquitin family	0.0036	24.0	1	124-195
1792	Gag_p10	Retroviral GAG p10 protein	4e-23	90.2	1	1-89
1798	Ribosomal_S12	Ribosomal protein S12	0.003	-14.2	1	7-66
1799	efhand	EF hand	1.1e-07	39.0	3	281-309:318-346:353-381
1799	Acyltransferase	Acyltransferase	0.0001	26.8	1	18-203
1801	zf-C2H2	Zinc finger, C2H2 type	3.2e-79	276.6	12	160-182:188-210:216-238:244-266:272-294:300-322:355-377:431-453:459-481:487-509:513-537:543-565
1801	LIM	LIM domain	4.7	-17.4	1	433-487
1802	lectin_c	Lectin C-type domain	1.4e-25	98.4	1	143-250
1802	lectin_c	Lectin C-type domain	1.4e-25	98.4	1	143-250
1804	efhand	EF hand	2.5e-08	41.1	2	16-44:56-82
1806	LRR	Leucine Rich Repeat	1.5e-07	38.5	5	130-151:152-173:174-195:196-217:221-243
1807	COX3	Cytochrome c oxidase subunit III	3.5	-233.2	1	51-219
1807	CblM	CblM	9.2	-93.3	1	114-249
1807	oxidored_q5_N	NADH-ubiquinone oxidoreductase chain 4	9.8	-59.5	1	89-169
1808	Sulfotransfer	Sulfotransferase protein	6.6	-108.5	1	39-282
1814	Metallophos	Calcineurin-like phosphoesterase	0.23	14.3	1	36-241
1815	rrm	RNA recognition motif	0.67	4.1	1	201-269
1816	filament	Intermediate filament protein	1.5	-188.9	1	1-253
1817	MAGE	MAGE family	4.2e-17	70.3	2	14-613:655-867
1817	Atrophin-I	Atrophin-I family	9.5	-684.8	1	4-783
1818	Tropomod	Tropomodulin	8.1	-168.0	1	362-653

SEQ ID	Model	Description	E-value	Score	Repeats	Position
	ulin					
1819	Hydrolase	haloacid dehalogenase-like hydrolase	3.4e-21	83.8	1	28-282
1820	Fe_hyd_l g_C	Iron only hydrogenase large subunit, C- te	1.3e-92	321.1	1	204-516
1820	Fe_hyd_S SU	Iron hydrogenase small subunit	8.3	-13.1	1	529-576
1821	filament	Intermediate filament protein	1e-143	490.8	1	55-366
1822	Keratin_B 2	Keratin, high sulfur B2 protein	0.082	-51.3	1	12-174
1824	metalthio	Metallothionein	5.7e-17	69.8	1	48-108
1824	AFP	Insect antifreeze protein	2.6	14.5	1	61-72
1825	C2	C2 domain	4.7e-53	189.7	2	373- 462:528- 617
1825	RPH3A_e ffector	Rabphilin-3A effector domain	0.035	-127.1	1	1-237
1825	zf-MIZ	MIZ zinc finger	0.4	-10.5	1	80-111
1825	PHD	PHD-finger	0.97	-9.7	1	62-108
1825	LJM	LJM domain	2.2	-14.6	1	80-128
1825	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	3.1	-4.0	1	63-105
1828	efhand	EF hand	8.4e-08	39.4	3	106- 134:142- 170:407- 435
1829	60s_ribos omal	60s Acidic ribosomal protein	7.4	-38.2	1	163-291
1831	Tektin	Tektin family	1.6	-227.3	1	1-150
1833	EGF	EGF-like domain	1.1e-32	122.0	5	26-54:57- 85:92- 124:156- 187:194- 226
1833	laminin_E GF	Laminin EGF-like (Domains III and V)	1.6	-5.9	1	29-63
1833	Bowman- Birk_leg	Bowman-Birk serine protease inhibitor	4.8	-16.7	1	37-85
1833	metalthio	Metallothionein	5.5	-10.1	1	59-117
1834	7tm_1	7 transmembrane receptor (rhodopsin family)	4.8e-05	-0.8	1	31-273
1834	7tm_2	7 transmembrane receptor (Secretin family)	5.5	-151.6	1	9-248
1835	rrm	RNA recognition motif	0.05	15.7	1	75-141
1835	Met_10	Met-10+ like-protein	0.065	-100.4	1	333-583
1835	UPF0020	Putative RNA methylase family UPF0020	0.073	-53.8	1	410-566
1835	PCMT	Protein-L-isopartate(D-aspartate) O-	0.2	-114.1	1	391-543
1835	Methyltra nsf_4	Putative methyltransferase	2.1	-82.0	1	424-566
1835	notch	Notch (DSL) domain	6.1	-10.5	1	233-271
1836	Kelch	Kelch motif	3e-33	123.9	4	242- 288:290- 331:333- 378:380- 435
1836	BTB	BTR/POZ domain	2.3	-15.2	1	1-129
1837	tsp_1	Thrombospondin type 1 domain	0.0014	23.3	5	139- 196:203- 256:257-

SEQ ID	Model	Description	E-value	Score	Repeats	Position
						313:320-370:374-432
1837	EB	EB module	6.4	-10.5	1	330-399
1838	adh_zinc	Zinc-binding dehydrogenase	7.3e-55	195.7	1	44-369
1838	Lipase_GDSL	Lipase/Acylhydrolase with GDSL-like motif	5.5	-20.4	1	103-189
1839	pkinase	Protein kinase domain	2.4e-05	-58.0	1	81-333
1841	zf-C2H2	Zinc finger, C2H2 type	4.4e-30	113.4	7	141-163:169-191:197-219:225-247:350-372:378-400:406-434
1841	KRAB	KRAB box	5.1e-23	89.9	1	44-84
1841	TFIIS	Transcription factor S-II (TFIIS)	2.4	-1.9	1	144-179
1841	Lentiviral_Tat	Lentiviral Tat protein	4.9	-23.0	1	35-125
1841	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	7.2	-7.1	1	352-411
1841	rubredoxin	Rubredoxin	7.4	-11.1	1	403-433
1842	E2F_TDP	Transcription factor E2F/dimerisation partner	1.5	-95.1	1	18-229
1843	V_ATPase_sub_a	V-type ATPase 116kDa subunit family	0	1258.7	1	26-831
1843	UCR_14kD	Ubiquinol-cytochrome C reductase complex	3.2	-40.4	1	6-112
1843	FlpP	FlpP family	4.8	-148.9	1	533-661
1843	PsbH	Photosystem II 10 kDa phosphoprotein	7.1	5.1	1	751-803
1844	na_permeases	Amino acid permease	5.6e-08	-125.3	1	28-529
1844	Aa_transpro	Transmembrane amino acid transporter	0.71	-178.9	1	30-408
1844	BPD_transport_2	Branched-chain amino acid transport system	3.3	-116.9	1	175-440
1844	MVIN	Virulence factor MVIN	3.5	-240.9	1	87-515
1844	FecCD	FecCD transport family	5.3	-216.0	1	311-521
1844	ion_trans	Ion transport protein	6.2	-11.7	1	288-493
1844	7tm_5	7TM chemoreceptor	7.1	-168.6	1	238-498
1848	sugar_tr	Sugar (and other) transporter	0.0072	-107.9	1	12-407
1848	xan_ur_permease	Permease family	5.6	-196.7	1	38-359
1848	FecCD	FecCD transport family	6.3	-217.4	1	56-287
1848	Nucleoside_transport	Nucleoside transporter	8.1	-162.4	1	82-365
1848	PUCC	PUCC protein	9.8	-283.2	1	51-403
1849	Filamin	Filamin/ABP280 repeat	2.3e-20	81.1	1	396-494
1849	zf-B_box	B-box zinc finger	9.3e-11	49.2	2	130-176:186-227
1849	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	0.0016	24.4	1	29-62
1853	ank	Ankyrin repeat	1.1e-98	341.3	10	485-517:518-550:551-583:584-616:617-

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						650:651- 683:684- 716:717- 749:750- 780:782- 814
1853	pkinese	Protein kinase domain	1.6e-50	181.3	1	22-286
1854	ras	Ras family	1.4e-13	17.8	1	5-194
1855	Acyltransf erase	Acyltransferase	3e-34	127.2	1	92-289
1856	wap	WAP-type (Whey Acidic Protein) four-disulf	0.0025	18.7	1	31-72
1857	arf	ADP-ribosylation factor family	2.5e-11	24.6	1	7-193
1857	GTP_EFT U	Elongation factor Tu GTP binding domain	1.6	-82.5	1	19-198
1858	zf-C2H2	Zinc finger, C2H2 type	2.1e-09	44.7	5	82- 104:110- 132:138- 161:164- 386:392- 416
1858	PHD	PHD-finger	7.7	-18.1	1	365-400
1859	zf-C2H2	Zinc finger, C2H2 type	7.2e-20	79.4	4	119- 141:147- 169:175- 198:214- 237
1860	BTB	BTB/POZ domain	1.7e-29	111.4	1	22-126
1860	zf-C2H2	Zinc finger, C2H2 type	5.1e-14	60.0	3	373- 395:401- 423:429- 452
1860	K_tetra	K+ channel tetramerisation domain	0.44	-30.2	1	34-124
1860	zf-BED	BED zinc finger	8.9	-6.9	1	363-396
1861	SNF2_N	SNF2 and others N-terminal domain	2.1e-72	254.0	1	137-473
1861	helicase C	Helicase conserved C-terminal domain	1.4e-24	95.1	1	559-632
1861	DEAD	DEAD/DEAH box helicase	0.26	-59.6	1	124-337
1861	SEC-C	SEC-C motif	0.43	13.8	1	426-446
1862	ras	Ras family	2.4e-69	263.8	1	19-217
1862	arf	ADP-ribosylation factor family	4.1e-05	-53.5	1	1-182
1864	rrm	RNA recognition motif	0.053	15.4	1	129-191
1867	T-box	T-box	4.3e-09	29.9	1	1-92
1870	F-box	F-box domain	1.8	15.0	1	124-171
1871	PH	PH domain	1.1e-13	58.9	1	170-273
1872	isodh	Isocitrate/isopropylmalate dehydrogenase	1.4e- 123	423.9	1	10-383
1873	ank	Ankyrin repeat	1.8e-08	41.5	2	39-71:72- 104
1874	ank	Ankyrin repeat	1.8e-08	41.5	2	67-99:100- 132
1875	PAP2	PAP2 superfamily	0.0034	13.0	1	1-107
1876	DUF51	Protein of unknown function DUF51	5.7e-13	52.5	1	107-261
1877	zf-C2H2	Zinc finger, C2H2 type	1.5e-72	254.5	9	285- 307:313- 335:341- 363:369- 391:397-

SEQ ID	Model	Description	E-value	Score	Repeats	Position
						419:425- 447:451- 473:479- 501:507- 529
1877	KRAB	KRAB box	2.7e-21	84.2	1	49-89
1877	zf-BED	BED zinc finger	0.74	2.7	1	344-392
1877	TFIIS	Transcription factor S-II (TFIIS)	1.5	-0.0	1	369-407
1877	GATA	GATA zinc finger	2.1	-7.1	1	477-524
1877	LIM	LIM domain	2.5	-15.1	1	371-435
1877	E6	Early Protein (E6)	5.7	-66.7	1	315-402
1878	AAA	ATPase family associated with various	1.3e-62	221.4	1	217-409
1878	Sigma54_activat	Sigma-54 interaction domain	4.6	-165.4	1	184-365
1879	SSF	Sodium:solute symporter family	4.8e-170	578.3	1	58-460
1880	SSF	Sodium:solute symporter family	1.3e-198	673.2	1	58-487
1881	perilipin	Perilipin family	6.7e-53	189.2	1	12-369
1882	aminotran_1_2	Aminotransferase class I and II	7.5e-07	25.0	1	165-515
1883	DSPc	Dual specificity phosphatase, catalytic domain	2.5e-30	114.2	1	54-199
1884	ig	Immunoglobulin domain	7.2e-14	59.5	2	34-111:155-229
1885	MCM	MCM2/3/5 family	4.6e-12	-67.3	1	106-391
1886	Kelch	Kelch motif	1.8e-63	224.3	6	262-306:309-356:358-403:405-453:455-495:497-544
1886	BTB	BTB/POZ domain	5.3e-32	119.7	1	26-134
1887	UBA	UBA/TS-N domain	1.9e-05	31.5	1	726-765
1887	rrm	RNA recognition motif.	0.00026	27.8	1	1342-1407
1887	MARCKS	MARCKS family	4.3	-90.8	1	270-571
1888	UBA	UBA/TS-N domain	1.9e-05	31.5	1	726-765
1888	rrm	RNA recognition motif.	0.00026	27.8	1	1303-1368
1888	MARCKS	MARCKS family	4.3	-90.8	1	270-571
1889	UBA	UBA/TS-N domain	1.9e-05	31.5	1	726-765
1889	rrm	RNA recognition motif.	0.00026	27.8	1	1245-1310
1889	MARCKS	MARCKS family	4.3	-90.8	1	270-571
1889	Atrophin-1	Atrophin-1 family	6.9	-676.1	1	237-986
1890	Na_H_Exchange	Sodium/hydrogen exchanger family	2.4e-18	74.4	1	119-520
1890	Na_Ca_Exch	Sodium/calcium exchanger protein	3.1	-43.6	1	270-384
1890	7tm_5	7TM chemoreceptor	3.8	-163.7	1	259-503
1890	Abi	CAAX amino terminal protease family	5.9	-25.8	1	309-401
1890	oxidored_q1	NADH-Ubiquinone/plastoquinone	7.9	-169.7	1	251-502
1891	Acyl-CoA_hydrolase	Cytosolic long-chain acyl-CoA thioesterase	8.9e-72	251.9	2	26-168:200-336
1891	tRNA_ant	OB-fold nucleic acid binding domain	3.5	5.8	1	230-307

SEQ ID	Model	Description	E-value	Score	Repeats	Position
	i					
1892	zf-DHHC	DHHC zinc finger domain	8.6e-18	72.5	1	145-207
1894	SPRY	SPRY domain	4.5e-11	50.2	1	353-474
1894	fn3	Fibronectin type III domain	0.054	17.6	1	165-258
1895	dsm	Double-stranded RNA binding motif	1.5e-12	55.1	2	229-293;337-401
1895	WW	WW domain	0.00016	28.5	1	20-49
1896	SPRY	SPRY domain	9.9e-26	98.9	1	186-301

TABLE 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
951	1c07	A	279	369	5.7e-21	0.77	1.00		EPIDERMAL GROWTH FACTOR RECEPTOR PATHWAY CHAIN: A;	SIGNALING PROTEIN CALCIUM BINDING, SIGNALING DOMAIN, NPF BINDING, FW BINDING, 2 EF-HAND, EH DOMAIN, SIGNALING PROTEIN
951	1c07	A	4	98	1.7e-07	-0.14	0.88		EPIDERMAL GROWTH FACTOR RECEPTOR PATHWAY CHAIN: A;	SIGNALING PROTEIN CALCIUM BINDING, SIGNALING DOMAIN, NPF BINDING, FW BINDING, 2 EF-HAND, EH DOMAIN, SIGNALING PROTEIN
951	1c11		293	345	3.8e-05	-0.02	0.22		CALCIUM-BINDING PROTEIN CALMODULIN (VERTEBRATE) ICLL 3	
951	1c12		278	369	1.1e-31	0.58	1.00		EPS15; CHAIN: NULL;	CALCIUM BINDING EH2, EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE CALCIUM BINDING, SIGNALING DOMAIN, NPF BINDING, EF-HAND, EH 2 DOMAIN
951	1c12	3	97	97	6.8e-11	0.72	0.99		EPS15; CHAIN: NULL;	CALCIUM BINDING EH2, EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE CALCIUM BINDING, SIGNALING DOMAIN, NPF BINDING, EF-HAND, EH 2 DOMAIN
951	1lro		280	348	1.3e-05	0.33	0.98		CALCIUM-BINDING PROTEIN RAT ONCOMODULIN IRRO 3	
951	1lre	A	284	345	1.5e-05	-0.21	0.23		CALCIUM BINDING PROTEIN CALMODULIN (/TR-2=CS FRAGMENT COMPRISING RESIDUES 78 - 148 ITRC 3 OF THE INTACT MOLECULE) ITRC 4	
951	1vrk	A	293	345	3.8e-05	-0.39	0.15		CALMODULIN; CHAIN: A; RS20; CHAIN: B;	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALING, 2 COMPLEX/CALCIUM-BINDING PROTEIN/PEPTIDE

SEQ ID NO:	PDB ID	CHAI ID	STAR T AA	END AA	Fsi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
951	2pvb	A	293	348	3.8e-05	-0.13	0.25		PARVALBUMIN; CHAIN: A;	METAL BINDING PROTEIN CALCIUM BINDING PROTEIN
951	2sep	A	283	345	5.7e-06	-0.13	0.47		BINDING PROTEIN SARCOPLASMIC CALCIUM- BINDING PROTEIN 2SCF 3	
952	1a75	A	310	389	0.00095	-0.81	0.05		PARVALBUMIN; CHAIN: A, B	CALCIUM BINDING PROTEIN CALCIUM BINDING PROTEIN, MUSCLE PROTEIN
952	1aj4		280	377	5.7e-05	0.02	0.17		TROPONIN C; CHAIN: NULL;	MUSCLE PROTEIN CTNC; CARDIAC, MUSCLE PROTEIN, REGULATORY, CALCIUM BINDING
952	1au1	B	280	377	0.00038	-0.03	0.13		SERINE/THREONINE PHOSPHATASE 2B; CHAIN: A, B;	HYDROLASE CALCINEURIN; HYDROLASE PHOSPHATASE, IMMUNOSUPPRESSION
952	1br1	B	282	377	0.0019	-0.05	0.18		MYOSIN; CHAIN: A, B, C, D, E, F, G, H;	MUSCLE PROTEIN MDE; MUSCLE PROTEIN
952	1bu3		310	389	0.0038	-0.24	0.05		CALCIUM-BINDING PROTEIN; CHAIN: NULL;	CALCIUM BINDING CALCIUM BINDING
952	1c07	A	279	369	5.7e-21	0.77	1.00		SIGNALING PROTEIN CALCIUM BINDING, SIGNALING DOMAIN, NPFF BINDING, FW BINDING, 2 EF-HAND, EH DOMAIN, SIGNALING PROTEIN	SIGNALING PROTEIN CALCIUM BINDING, SIGNALING DOMAIN, NPFF BINDING, FW BINDING, 2 EF-HAND, EH DOMAIN, SIGNALING PROTEIN
952	1c07	A	4	99	5.1e-12	0.10	0.90		EPIDERMAL GROWTH FACTOR RECEPTOR PATHWAY CHAIN: A;	EPIDERMAL GROWTH FACTOR RECEPTOR PATHWAY CHAIN: A;
952	1ell		293	345	3.8e-05	-0.02	0.22		CALCIUM-BINDING PROTEIN CALMODULIN (VERTEBRATE) ICL1.3	
952	1dh	A	280	389	0.0038	-0.16	0.18		CARDIAC TROPONIN C; CHAIN: A;	STRUCTURAL PROTEIN HELIX- TURN-HELIX
952	1eh2		278	369	1.1e-31	0.58	1.00		EPH15; CHAIN: NULL;	CALCIUM BINDING EPH2, EPIDERMAL GROWTH FACTOR

SEQ ID NO:	PDB ID	CHAI ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
952	1eh2		3	97	1.7e-13	0.81	0.99		EPS15; CHAIN: NULL;	RECEPTOR SUBSTRATE CALCIUM BINDING, SIGNALING DOMAIN, NPF BINDING, EF-HAND, EH 2 DOMAIN
952	1gdf	A	14	97	1.7e-08	0.64	0.80		EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE CALCIUM BINDING, SIGNALING DOMAIN, NPF BINDING, EF-HAND, EH 2 DOMAIN	CALCIUM BINDING EH2, EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE CALCIUM BINDING, SIGNALING DOMAIN, NPF BINDING, EF-HAND, EH 2 DOMAIN
952	1rrr		280	348	1.3e-05	0.33	0.98		EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE CHAIN: A;	GROWTH FACTOR EHF: EH DOMAIN, EPS15, EF-HAND, SOLUTION STRUCTURE, S100 PROTEIN
952	1trc	A	284	345	1.5e-05	-0.21	0.23		CALCIUM-BINDING PROTEIN RAT ONCOMODULIN 1RRO 3 CALCIUM BINDING PROTEIN CALMODULIN (TR-2-CS) FRAGMENT COMPRISING RESIDUES 78 - 148 1TRC 3 OF THE INTACT MOLECULE) 1TRC 4	
952	1vrk	A	280	377	0.00038	-0.23	0.49		CALMODULIN; CHAIN: A; RS20; CHAIN: B;	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)
952	1vrk	A	293	345	3.8e-05	-0.39	0.15		CALMODULIN; CHAIN: A; RS20; CHAIN: B;	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)
952	2pvh	A	293	348	3.8e-05	-0.13	0.25		PARVALBUMIN; CHAIN: A;	CALCIUM BINDING PROTEIN
952	2sep	A	283	345	5.7e-06	-0.13	0.47		BINDING PROTEIN SARCOPLASMIC CALCIUM-BINDING PROTEIN 2SCP 3	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
953	1a09	A	319	413	3.8e-17	0.34	0.98		C-SRC TYROSINE KINASE; CHAIN: A, B; ACE-FORMYL PHOSPHOTYR-GLU-(N,N-DIPENTYL AMINE); CHAIN: C, D;	COMPLEX (TRANSFERASE/PEPTIDE) COMPLEX (TRANSFERASE/PEPTIDE)
953	1a81	A	255	413	1.5e-18	0.27	0.72		SYK KINASE; CHAIN: A, C, E, G, I, K; T-CELL SURFACE GLYCOPROTEIN CD3 EPSILON; CHAIN: B, D, F, H, J, L;	COMPLEX (TRANSFERASE/PEPTIDE) ITAM PEPTIDE; COMPLEX (TRANSFERASE/PEPTIDE), SYK, KINASE, SH2 DOMAIN, ITAM
953	1a62		319	417	3.8e-17	0.02	0.63		TRANSFERASE/PHOSPHOTRANSFERASE) PROTO-ONCOGENE TYROSINE KINASE (E.C.2.7.1.112) IAB2 3 (SRC HOMOLOG 2 DOMAIN) (ABELSON, SH2 ABL) IAB2 4 (NMR, 20 STRUCTURES) IAB2 5	
953	1a08	F	319	413	1.7e-17	0.46	0.99		FYN PROTEIN-TYROSINE KINASE; CHAIN: F; PHOSPHOTYROSYL PEPTIDE; CHAIN: P	COMPLEX (PROTO-ONCOGENE/EARLY PROTEIN) SRC HOMOLOG 2 DOMAIN; SH2 DOMAIN; SIGNAL TRANSDUCTION, PEPTIDE COMPLEX, 2 COMPLEX (PROTO-ONCOGENE/EARLY PROTEIN)
953	1aya	A	317	412	7.6e-18	0.18	1.00		HYDROLASE (SH2 DOMAIN) TYROSINE PHOSPHATASE SYP (N-TERMINAL SH2 DOMAIN) IAYA 3 (PTPID, SHPTP2) (E.C.3.1.3.48) COMPLEXED WITH THE PEPTIDE IAYA 4 PDGFR-1009 IAYA 5	
953	1b0f		319	418	3.8e-19	0.36	0.82		P85 ALPHA; CHAIN: NULL;	SH2 DOMAIN PHOSPHATIDYLINOSITOL 3-KINASE REGULATORY ALPHA SH2

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQOL D score	Compound	PDB annotation
953	1asy	A	319	416	3.8e-19	0.33	0.82		SYK PROTEIN TYROSINE KINASE; CHAIN: A; ACETYL-THR-PTG-GLU-THR-LEU-NH ₂ ; CHAIN: B;	DOMAIN: P85ALPHA, PT 3-KINASE, NMR, C-TERMINAL SH2 2 DOMAIN COMPLEX (PHOSPHOTRANSFERASE/PEPTIDE) PROTEIN-TYROSINE KINASE SH2 DOMAIN, COMPLEX 2
953	1eum	A	140	228	0.00013	0.05	0.06		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
953	1dlz	B	320	413	5.7e-18	0.04	0.49		SAP SH2 DOMAIN; CHAIN: A, B, C, D;	GENE REGULATION SH2 DOMAINS
953	1d4t	A	319	413	1.9e-19	0.22	0.75		T CELL SIGNAL TRANSDUCTION MOLECULE SAP; CHAIN: A; SIGNALING LYMOPHYTIC ACTIVATION MOLECULE; CHAIN: B;	SIGNALING PROTEIN SLAM, SH2 DOMAIN, TYROSINE KINASE, SIGNAL TRANSDUCTION, PEPTIDE 2 RECOGNITION
953	1lfs		312	425	0.0017		58.62		GROWTH FACTOR RECEPTOR BOUND PROTEIN-2; CHAIN: NULL;	SH2 DOMAIN GRB2; GRB2, SH2 DOMAIN, PROTEIN NMR, SOLUTION STRUCTURES
953	2pld	A	319	417	9.5e-19	0.32	0.49		PHOSPHORIC DIESTER HYDROLASE PHOSPHOLIPASE C-GAMMA-1 (E.C.3.1.4.11) (C-TERMINAL SH2 2PLD 3 DOMAIN COMPRISING RESIDUES 663 - 759) COMPLEXED WITH A 2PLD 4 PHOSPHOPEPTIDE FROM THE PLATELET-DERIVED GROWTH FACTOR 2PLD 5 RECEPTOR (RESIDUES 1018 - 1029): ASP-ASN-ASP-PTYR-ILE-ILE-2PLD 6	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQOL D score	Compound	PDB annotation
									PRO-LEU-PRO-ASP-PRO-LYS (NMR, MINIMIZED AVERAGE STRUCTURE) 2PLD 7	
954	1a09	A	346	440	3.8e-17	0.34	0.98		C-SRC TYROSINE KINASE; CHAIN: A, B; ACE-FORMYL PHOSPHOTYR-GLU-N'-DIPENTYL AMINE; CHAIN: C, D;	COMPLEX (TRANSFERASE/PEPTIDE) COMPLEX (TRANSFERASE/PEPTIDE)
954	1a81	A	252	440	1.5e-18	0.27	0.72		SYK KINASE; CHAIN: A, C, E, G, I, K; T-CELL SURFACE GLYCOPROTEIN CD3 EPSILON CHAIN; CHAIN: B, D, F, H, J, L;	COMPLEX (TRANSFERASE/PEPTIDE) ITAM PEPTIDE; COMPLEX (TRANSFERASE/PEPTIDE) SYK, KINASE, SH2 DOMAIN, ITAM
954	1a02		346	444	3.8e-17	0.02	0.63		TRANSFERASE (PHOSPHOTRANSFERASE) PROTO-ONCOGENE TYROSINE KINASE (E.C.2.7.1.112) IAB2 3 (SRC HOMOLOG 2 DOMAIN) (ABELSON, SH2 ABL) IAB2 4 (NMR, 20 STRUCTURES) IAB2 5	
954	1a01	F	346	440	1.7e-17	0.46	0.99		FYN PROTEIN-TYROSINE KINASE; CHAIN: F; PHOSPHOTYROSYL PEPTIDE; CHAIN: P	COMPLEX (PROTO-ONCOGENE/EARLY PROTEIN) SRC HOMOLOG 2 DOMAIN; SH2 DOMAIN, SIGNAL TRANSDUCTION, PEPTIDE, COMPLEX, 2 COMPLEX (PROTO-ONCOGENE/EARLY PROTEIN)
954	1a1a	A	344	439	7.6e-18	0.18	1.00		HYDROLASE (SH2 DOMAIN) TYROSINE PHOSPHATASE SYP (N-TERMINAL SH2 DOMAIN) IAYA 3 (PTP ID, SHPTP2) (E.C.3.1.3.48) COMPLEXED WITH THE PEPTIDE IAYA 4	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
954	1bfi		346	445	3.8e-19	0.36	0.82		PDGFR-1009 IAYA 5 T85 ALPHA; CHAIN: NULL;	SH2 DOMAIN PHOSPHATIDYLINOSITOL 3-KINASE REGULATORY ALPHA SH2 DOMAIN; P85ALPHA; P13-KINASE, NMR, C-TERMINAL SH2 2 DOMAIN COMPLEX
954	1esy	A	346	443	3.8e-19	0.33	0.82		SYK PROTEIN TYROSINE KINASE; CHAIN: A; ACETYL- THR-PTT-GLU-THR-LEU-NH2; CHAIN: B;	(PHOSPHOTRANSFERASE/PEPTIDE) PROTEIN-TYROSINE KINASE SH2 DOMAIN, COMPLEX 2 (PHOSPHOTRANSFERASE/PEPTIDE) GENE REGULATION SH2 DOMAINS
954	1dlz	B	347	440	5.7e-18	0.04	0.49		SAP SH2 DOMAIN; CHAIN: A, B, C, D;	SIGNALING PROTEIN SLAMF SH2 DOMAIN, TYROSINE KINASE, SIGNAL TRANSDUCTION, PEPTIDE 2 RECOGNITION
954	1d4e	A	346	440	1.9e-19	0.22	0.75		T CELL SIGNAL TRANSDUCTION MOLECULE SAP; CHAIN: A; SIGNALING LYMPHOCYTIC ACTIVATION MOLECULE; CHAIN: B;	PHOSPHORIC DIESTER HYDROLASE PHOSPHOLIPASE C-GAMMA-1 (E.C.3.1.4.11) (C- TERMINAL SH2 2PLD 3 DOMAIN COMPRISING RESIDUES 663 - 759) COMPLEXED WITH A 2PLD 4 PHOSPHOPEPTIDE FROM THE PLATELET-DERIVED GROWTH FACTOR 2PLD 5 RECEPTOR (RESIDUES 1018 - 1029; ASP, ASN-ASP-PTYR-ILE-LEU-2PLD 6 PRO-LEU-PRO-ASP-PRO-ALYS (NMR, MINIMIZED AVERAGE STRUCTURE) 2PLD 7
954	2pld	A	346	444	9.5e-19	0.32	0.49			

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQ/OL D score	Compound	PDB annotation
955	1a12	A	35	427	1.7e-77			150.38	REGULATOR OF CHROMOSOME CONDENSATION I; CHAIN: A, B, C;	GUANINE NUCLEOTIDE EXCHANGE FACTOR RCCI; GUANINE NUCLEOTIDE EXCHANGE FACTOR, GEF, RAN, 2 RAS-LIKE NUCLEAR GTP-BINDING PROTEIN HEADER
955	1a12	A	51	423	1.7e-77	0.69	1.00		REGULATOR OF CHROMOSOME CONDENSATION I; CHAIN: A, B, C;	GUANINE NUCLEOTIDE EXCHANGE FACTOR RCCI; GUANINE NUCLEOTIDE EXCHANGE FACTOR, GEF, RAN, 2 RAS-LIKE NUCLEAR GTP-BINDING PROTEIN HEADER
957	1azw	A	85	183	0.0076	-0.16	0.05		PROLINE IMINOPEPTIDASE; CHAIN: A, B;	AMINOPEPTIDASE IMINOPEPTIDASE, PROLINE IMINOPEPTIDASE, SERINE PROTEASE, 2 XANTHOMONAS CAMPESTRIS
957	1evl		166	204	0.00038	-0.67	0.49		TRIACYLGLYCEROL HYDROLASE; CHAIN: NULL;	HYDROLASE, X-RAY CRYSTALLOGRAPHY, 2 PSEUDOMONADACEAE, OXYANION, CIS-PEPTIDE, HYDROLASE
957	1e9	A	86	204	7.6e-05	0.14	0.57		PALMITOYL PROTEIN THIOESTERASE I; CHAIN: A;	HYDROLASE, GLYCOPROTEIN
957	4lip	D	165	204	0.0048	-0.60	0.23		TRIACYL-GLYCEROL-HYDROLASE; CHAIN: D, E;	LIPASE LIPASE; LIPASE, HYDROLASE, PSEUDOMONADACEAE, COVALENT INTERMEDIATE, 2 TRIGLYCERIDE ANALOGUE, ENANTIOSELECTIVITY
962	1ayz	A	2	121	3.8e-38	0.57	1.00		UBIQUITIN-CONJUGATING ENZYME RAD6; CHAIN: A, B, C;	UBIQUITIN CONJUGATION UBC2; UBIQUITIN CONJUGATION,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
962	1ayz	A	2	121	3.8e-38			124.83	UBIQUITIN-CONJUGATING ENZYME	UBIQUITIN-CONJUGATING ENZYME
962	1ayz	A	2	121	5.1e-37	0.63	1.00		UBIQUITIN-CONJUGATING ENZYME RAD6; CHAIN: A, B, C;	UBIQUITIN CONJUGATION, UBIQUITIN-CONJUGATING ENZYME
962	1qcc	A	1	119	3.4e-40	0.62	1.00		UBIQUITIN-CONJUGATING ENZYME RAD6; CHAIN: A, B, C;	UBIQUITIN CONJUGATION, UBIQUITIN-CONJUGATING ENZYME
962	1qcc	A	3	120	3.4e-40			70.02	UBIQUITIN CONJUGATING ENZYME; CHAIN: A;	LIGASE UBIQUITIN, UBIQUITIN-CONJUGATING ENZYME, YEAST
962	2auk		1	119	3.4e-37	0.59	1.00		UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	UBIQUITIN CONJUGATION, UBIQUITIN-CONJUGATING ENZYME, YEAST
962	2auk		1	120	3.4e-37			141.95	UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	UBIQUITIN CONJUGATION, UBIQUITIN-CONJUGATING ENZYME, YEAST
963	1ayz	A	2	136	1.5e-46	1.15	1.00		UBIQUITIN-CONJUGATING ENZYME RAD6; CHAIN: A, B, C;	UBIQUITIN CONJUGATION, UBIQUITIN-CONJUGATING ENZYME
963	1ayz	A	2	136	1.9e-48	0.91	1.00		UBIQUITIN-CONJUGATING ENZYME RAD6; CHAIN: A, B, C;	UBIQUITIN CONJUGATION, UBIQUITIN-CONJUGATING ENZYME
963	1ayz	A	2	136	1.9e-48			162.79	UBIQUITIN-CONJUGATING ENZYME RAD6; CHAIN: A, B, C;	UBIQUITIN CONJUGATION, UBIQUITIN-CONJUGATING ENZYME
963	1qcc	A	1	134	1.5e-50	0.63	1.00		UBIQUITIN CONJUGATING ENZYME; CHAIN: A;	LIGASE UBIQUITIN, UBIQUITIN-CONJUGATING ENZYME, YEAST
963	1qcc	A	3	135	1.5e-50			102.58	UBIQUITIN CONJUGATING ENZYME; CHAIN: A;	LIGASE UBIQUITIN, UBIQUITIN-CONJUGATING ENZYME, YEAST

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
963	2auk		1	134	3.4e-48	0.88	1.00		ENZYME; CHAIN: A; UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	CONJUGATING ENZYME, YEAST UBIQUITIN CONJUGATION UBC1; UBIQUITIN CONJUGATION LIGASE
963	2auk		1	135	3.4e-48			179.88	UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	UBIQUITIN CONJUGATION UBC1; UBIQUITIN CONJUGATION LIGASE
971	1bg2		6	371	0			207.35	KINESIN; CHAIN: NULL;	MOTOR PROTEIN MOTOR PROTEIN, ATPASE, MICROTUBULE ASSOCIATED
971	1bg2		7	371	0	0.39	1.00		KINESIN; CHAIN: NULL;	MOTOR PROTEIN MOTOR PROTEIN, ATPASE, MICROTUBULE ASSOCIATED
971	1ez7	A	5	372	1.7e-81	0.33	1.00		MICROTUBULE MOTOR PROTEIN NCD; CHAIN: A, B, C, D;	CONTRACTILE PROTEIN NCD, CLARET SEGREGATIONAL PROTEIN; NCD CRYSTAL STRUCTURE, MICROTUBULE MOTORS, KINESIN 2 SUPERFAMILY, CONTRACTILE PROTEIN
971	1ez7	A	7	372	1.7e-98			139.50	MICROTUBULE MOTOR PROTEIN NCD; CHAIN: A, B, C, D;	CONTRACTILE PROTEIN NCD, CLARET SEGREGATIONAL PROTEIN; NCD CRYSTAL STRUCTURE, MICROTUBULE MOTORS, KINESIN 2 SUPERFAMILY, CONTRACTILE PROTEIN
971	1ez7	A	9	372	1.7e-98	0.34	1.00		MICROTUBULE MOTOR PROTEIN NCD; CHAIN: A, B, C, D;	CONTRACTILE PROTEIN NCD, CLARET SEGREGATIONAL PROTEIN; NCD CRYSTAL STRUCTURE, MICROTUBULE MOTORS, KINESIN 2 SUPERFAMILY, CONTRACTILE PROTEIN
971	1dm1	B	647	825	1.3e-15	0.15	-0.18		SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1A; CHAIN: B;	ENDOCYTOSIS/EXOCYTOSIS NSEC; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT
971	1eri	A	1269	1643	1.7e-78	0.54	0.98		TRANSCRIPTIONAL	TRANSCRIPTION INHIBITOR BETA-

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									REPRESSOR TUPI; CHAIN: A; B, C;	PROPELLER
971	1got	B	1229	1600	1e-98			113.67	GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION
971	1got	B	1317	1640	1e-98	0.88	1.00		GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION
971	1got	B	1429	1660	3.4e-46	0.42	1.00		GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION
971	2kin	A	3	260	1.5e-71			135.00	KINESIN; CHAIN: A; B;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
971	2kin	A	7	281	1.5e-71	0.09	1.00		KINESIN; CHAIN: A; B;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
971	2kin	B	296	380	1.7e-36	-0.48	0.99		KINESIN; CHAIN: A; B;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
971	2ncd	A	5	370	1e-81	0.34	1.00		KINESIN MOTOR NCD; CHAIN: A;	CONTRACTILE PROTEIN KINESIN, MICROTUBULE-BASED MOTOR,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
971	2ned	A	7	371	1e-81			132.55	KINESIN MOTOR NCD; CHAIN: A;	NCD, CONTRACTILE PROTEIN CONTRACTILE PROTEIN KINESIN, MICROTUBULE-BASED MOTOR, NCD, CONTRACTILE PROTEIN
971	3kar		8	370	1.9e-91			165.99	KINESIN-LIKE PROTEIN KAR3; CHAIN: NULL;	CONTRACTILE PROTEIN CONTRACTILE PROTEIN, KAR3, KINESIN-RELATED PROTEIN, MOTOR 2 PROTEIN, ATPASE, P-LOOP, MICROTUBULE BINDING PROTEIN
971	3kar		8	370	1e-83	0.30	1.00		KINESIN-LIKE PROTEIN KAR3; CHAIN: NULL;	CONTRACTILE PROTEIN CONTRACTILE PROTEIN, KAR3, KINESIN-RELATED PROTEIN, MOTOR 2 PROTEIN, ATPASE, P-LOOP, MICROTUBULE BINDING PROTEIN
971	3kar		9	370	1.9e-91	0.19	1.00		KINESIN-LIKE PROTEIN KAR3; CHAIN: NULL;	CONTRACTILE PROTEIN CONTRACTILE PROTEIN, KAR3, KINESIN-RELATED PROTEIN, MOTOR 2 PROTEIN, ATPASE, P-LOOP, MICROTUBULE BINDING PROTEIN
971	3kln	B	298	380	3.8e-35	-0.23	1.00		KINESIN HEAVY CHAIN; CHAIN: A, B, C, D;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
971	3kln	B	298	405	6.8e-28	-0.39	1.00		KINESIN HEAVY CHAIN; CHAIN: A, B, C, D;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
975	1huo	A	5	125	1.7e-20	0.20	1.00		PROMYELOCYTIC LEUKEMIA ZINC FINGER PROTEIN PLZF; CHAIN: A;	GENE REGULATION POZ DOMAIN; PROTEIN-PROTEIN INTERACTION DOMAIN, TRANSCRIPTIONAL 2 REPRESSOR, ZINC-FINGER PROTEIN, X-RAY CRYSTALLOGRAPHY, 3 PROTEIN STRUCTURE, PROMYELOCYTIC

SEQ NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
975	1huo	A	5	128	3.8e-28	0.41	0.99		PROMYELOCYTIC LEUKEMIA ZINC FINGER PROTEIN PLZF; CHAIN: A;	LEUKEMIA, GENE REGULATION GENE REGULATION POZ DOMAIN; PROTEIN-PROTEIN INTERACTION DOMAIN, TRANSCRIPTIONAL 2 REPRESSOR, ZINC-FINGER PROTEIN, X-RAY CRYSTALLOGRAPHY, 3 PROTEIN STRUCTURE, PROMYELOCYTIC LEUKEMIA, GENE REGULATION
975	1huo	A	5	130	3.8e-28			58.76	PROMYELOCYTIC LEUKEMIA ZINC FINGER PROTEIN PLZF; CHAIN: A;	GENE REGULATION POZ DOMAIN; PROTEIN-PROTEIN INTERACTION DOMAIN, TRANSCRIPTIONAL 2 REPRESSOR, ZINC-FINGER PROTEIN, X-RAY CRYSTALLOGRAPHY, 3 PROTEIN STRUCTURE, PROMYELOCYTIC LEUKEMIA, GENE REGULATION
975	1gof		251	464	0.0022	0.10	0.19		OXIDOREDUCTASE(OXYGEN)(A) GALACTOSE OXIDASE (E.C.1.1.3.9) (PH 4.5) IGO F 3	
975	1gof		288	385	5.1e-10	0.03	-0.02		OXIDOREDUCTASE(OXYGEN)(A) GALACTOSE OXIDASE (E.C.1.1.3.9) (PH 4.5) IGO F 3	
977	1bg2		1	352	6.8e-81			220.57	KINESIN; CHAIN: NULL;	MOTOR PROTEIN MOTOR PROTEIN, ATPASE, MICROTUBULE ASSOCIATED
977	1bg2		2	352	6.8e-81	0.74	1.00		KINESIN; CHAIN: NULL;	MOTOR PROTEIN MOTOR PROTEIN, ATPASE, MICROTUBULE ASSOCIATED
977	1ez7	A	3	352	8.5e-69			160.51	MICROTUBULE MOTOR PROTEIN NCD; CHAIN: A, B, C, D;	CONTRACTILE PROTEIN NCD, CLARET SEGREGATIONAL PROTEIN; NCD CRYSTAL STRUCTURE, MICROTUBULE

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
977	1c27	A	5	354	8.5e-69	0.58	1.00		MICROTUBULE MOTOR PROTEIN NCD; CHAIN: A, B, C, D;	MOTORS, KINESIN 2 SUPERFAMILY, CONTRACTILE PROTEIN CONTRACTILE PROTEIN NCD, CLARET SEGREGATIONAL PROTEIN, NCD CRYSTAL STRUCTURE, MICROTUBULE MOTORS, KINESIN 2 SUPERFAMILY, CONTRACTILE PROTEIN
977	1dm1	B	365	430	5.7e-05	0.21	0.16		SYNTAXIN BINDING PROTEIN I; CHAIN: A; SYNTAXIN 1A; CHAIN: B;	ENDOCYTOSIS/EXOCYTOSIS NSEC; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT
977	1f1o	A	582	766	0.0057	-0.00	0.10		SSO1 PROTEIN; CHAIN: A;	MEMBRANE PROTEIN FOUR HELIX BUNDLE, ALPHA HELIX
977	2kin	A	1	259	5.2e-72			151.15	KINESIN; CHAIN: A, B;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
977	2kin	A	1	259	5.7e-72			151.15	KINESIN; CHAIN: A, B;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
977	2kin	A	2	258	1.2e-55	0.38	1.00		KINESIN; CHAIN: A, B;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
977	2kin	A	2	259	5.7e-72	0.45	1.00		KINESIN; CHAIN: A, B;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
977	2kin	B	272	366	1.7e-17	-0.24	1.00		KINESIN; CHAIN: A, B;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
977	2kin	B	274	364	1.9e-36	-0.22	1.00		KINESIN; CHAIN: A, B;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
977	2ncd	A	3	352	1.2e-68			157.70	KINESIN MOTOR NCD; CHAIN: A;	CONTRACTILE PROTEIN KINESIN, MICROTUBULE-BASED MOTOR, NCD, CONTRACTILE PROTEIN
977	2ncd	A	5	346	1.2e-68	0.64	1.00		KINESIN MOTOR NCD; CHAIN: A;	CONTRACTILE PROTEIN KINESIN, MICROTUBULE-BASED MOTOR, NCD, CONTRACTILE PROTEIN
977	3kar		4	351	3.4e-66			182.54	KINESIN-LIKE PROTEIN KAR3; CHAIN: NULL;	CONTRACTILE PROTEIN, KAR3, KINESIN-RELATED PROTEIN,

SEQ ID NO:	PDE ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										MOTOR 2 PROTEIN, ATPASE, P-LOOP, MICROTUBULE BINDING PROTEIN
977	3kar		5	348	3.4e-66	0.58	1.00		KINESIN-LIKE PROTEIN KAR3; CHAIN: NULL;	CONTRACTILE PROTEIN KINESIN-RELATED PROTEIN, MOTOR 2 PROTEIN, ATPASE, P-LOOP, MICROTUBULE BINDING PROTEIN
977	3kin	B	276	364	1.5e-34	-0.10	0.99		KINESIN HEAVY CHAIN; CHAIN: A, B, C, D;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
977	3kin	B	276	366	1e-16	-0.19	1.00		KINESIN HEAVY CHAIN; CHAIN: A, B, C, D;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
982	1aut	L	597	670	1.5e-10	0.03	-0.19		ACTIVATED PROTEIN C; CHAIN: C, L; D-PHE-PRO-MAL; CHAIN: P;	COMPLEX (BLOOD COAGULATION/INHIBITOR) AUTOPROTHROMBIN IIA; HYDROLASE, SERINE PROTEINASE, PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD COAGULATION/INHIBITOR)
982	1aut	L	745	823	1.1e-24	0.36	0.41		ACTIVATED PROTEIN C; CHAIN: C, L; D-PHE-PRO-MAL; CHAIN: P;	COMPLEX (BLOOD COAGULATION/INHIBITOR) AUTOPROTHROMBIN IIA; HYDROLASE, SERINE PROTEINASE, PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD COAGULATION/INHIBITOR)
982	1oej	A	740	820	1.9e-20	-0.11	0.16		MEROZOITE SURFACE PROTEIN 1; CHAIN: A;	SURFACE PROTEIN MEROZOITE SURFACE ANTIGEN 1, MAJOR BLOOD-STAGE EGG-LIKE DOMAIN, EXTRACELLULAR, MODULAR

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
										PROTEIN SURFACE 2 ANTIGEN, MALARIA VACCINE COMPONENT, SURFACE PROTEIN
982	1ckl	A	3	107	1.9e-16	0.22	0.17		CD46; CHAIN: A, B, C, D, E, F;	GLYCOPROTEIN MEMBRANE COFACTOR PROTEIN (MCP) VIRUS RECEPTOR, COMPLEMENT COFACTOR, SHORT CONSENSUS REPEAT, 2 SCR, MEASLES VIRUS, GLYCOPROTEIN
982	1d4v	A	556	658	5.7e-09	0.29	-0.12		TNF-RELATED APOPTOSIS INDUCING LIGAND; CHAIN: B; DEATH RECEPTOR 5; CHAIN: A;	APOPTOSIS TRAIL; DR5; LIGAND-RECEPTOR COMPLEX, TRIMERIC JELLY-ROLL, TNF-R 2 SUPERFAMILY, APOPTOSIS
982	1dan	L	738	823	6.8e-16	0.13	0.11		BLOOD COAGULATION FACTOR VILIA; CHAIN: L, H; SOLUBLE TISSUE FACTOR; CHAIN: T; U; D-PHE-PHE-ARG-CHLOROMETHYLKETONE (DIFFROMK) WITH CHAIN: C;	BLOOD COAGULATION, SERINE PROTEASE, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)
982	1dan	L	741	831	1.1e-24	-0.19	0.27		BLOOD COAGULATION FACTOR VILIA; CHAIN: L, H; SOLUBLE TISSUE FACTOR; CHAIN: T; U; D-PHE-PHE-ARG-CHLOROMETHYLKETONE (DIFFROMK) WITH CHAIN: C;	BLOOD COAGULATION, SERINE PROTEASE, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)
982	1dan	L	759	846	3.8e-24	-0.16	0.00		BLOOD COAGULATION FACTOR VILIA; CHAIN: L, H; SOLUBLE TISSUE FACTOR; CHAIN: T; U; D-PHE-PHE-ARG-CHLOROMETHYLKETONE (DIFFROMK) WITH CHAIN: C;	BLOOD COAGULATION, SERINE PROTEASE, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)
982	1dva	L	734	831	3.8e-23	-0.18	0.00		DES-GLA FACTOR VILIA (HEAVY CHAIN); CHAIN: H, I; DES-GLA FACTOR VILIA (LIGHT	HYDROLASE/HYDROLASE INHIBITOR PROTEIN-PEPTIDE COMPLEX

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fsi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									CHAIN: L, M; (DPN)-PHE-ARG; CHAIN: C, D; PEPTIDE E-76; CHAIN: X, Y;	
982	1dva	L	738	823	6.8e-16	-0.02	0.13		DES-GLA FACTOR VIIA (HEAVY CHAIN); CHAIN: H, I; DES-GLA FACTOR VIIA (LIGHT CHAIN); CHAIN: L, M; (DPN)-PHE-ARG; CHAIN: C, D; PEPTIDE E-76; CHAIN: X, Y; COMPLEMENT CONTROL	HYDROLASE/HYDROLASE INHIBITOR PROTEIN-PEPTIDE COMPLEX
982	1e5g	A	3	96	3.8e-17	0.18	0.33		PROTEIN; CHAIN: A;	COMPLEMENT INHIBITOR YCP, SP35; COMPLEMENT, NMR, MODULES, PROTEIN STRUCTURE, VACCINIA VIRUS
982	1enn		237	337	1.7e-11	0.09	-0.19		FIBRILLIN; CHAIN: NULL;	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN
982	1enn		738	809	3.4e-15	-0.22	0.06		FIBRILLIN; CHAIN: NULL;	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN
982	1ext	A	533	672	1.9e-10	0.07	0.01		TUMOR NECROSIS FACTOR RECEPTOR; CHAIN: A, B;	SIGNALING PROTEIN BINDING PROTEIN, CYTOKINE, SIGNALING PROTEIN
982	1l7e	A	741	781	5.7e-17	0.15	0.75		BLOOD COAGULATION FACTOR VII; CHAIN: A;	BLOOD CLOTTING FACTOR VII, BLOOD COAGULATION, EGF-LIKE

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	FMF score	SEQFOL D score	Compound	PDB annotation
982	1hfh		2	96	9.5e-16	0.03	0.23		GLYCOPROTEIN FACTOR H _{15TH} AND 16TH C-MODULE PAIR (NMR, MINIMIZED 1HFA 1 AVERAGED STRUCTURE)	DOMAIN, BLOOD 2 CLOTTING
982	1pfx	L	741	840	1.3e-32	-0.03	0.11		FACTOR IXA; CHAIN: C, L ₁ ; D-PHE-PRO-ARG; CHAIN: I ₁	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
982	1qfk	L	741	830	3.8e-29	0.01	0.05		COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L ₁ ; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H ₁ ; TRIPEPTIDYL INHIBITOR; CHAIN: G ₁	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE
982	1wve		2	96	1.7e-14	0.18	-0.09		VACCINIA VIRUS COMPLEMENT CONTROL PROTEIN; CHAIN: NULL ₁	COMPLEMENT INHIBITOR SP35, VCP, VACCINIA VIRUS SP35; COMPLEMENT INHIBITOR, COMPLEMENT MODULE, SCR, SUSHI DOMAIN, 2 MODULE PAIR
982	1whe		744	814	1.1e-19	-0.30	0.11		COAGULATION FACTOR X; CHAIN: NULL ₁	GLYCOPROTEIN GLYCOPROTEIN, HYDROLASE, SERINE PROTEASE, PLASMA, BLOOD 2 COAGULATION FACTOR
982	1xka	L	369	441	5.1e-10	0.04	-0.13		BLOOD COAGULATION FACTOR XA; CHAIN: L ₁ ; C ₁	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	FMF score	SEQPOL D score	Counpound	PDB annotation
982	1xka	L	741	831	1.9e-27	0.05	0.06		BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN
982	4m2		557	617	1.4e-09	-0.46	0.07		METALLOTHIONEIN METALLOTHIONEIN ISOFORM II 4MT2.3	
986	1a6a	B	22	202	1.4e-46			61.03	HLA-DR3; CHAIN: A, B; CLIP; CHAIN: C;	COMPLEX (TRANSMEMBRANE/GLYCOPROTEIN) MHC GLYCOPROTEIN, COMPLEX (TRANSMEMBRANE/GLYCOPROTEIN)
986	1a6a	B	25	201	1.4e-46	-0.06	0.39		HLA-DR3; CHAIN: A, B; CLIP; CHAIN: C;	COMPLEX (TRANSMEMBRANE/GLYCOPROTEIN) MHC GLYCOPROTEIN, COMPLEX (TRANSMEMBRANE/GLYCOPROTEIN)
986	1aqp	B	16	201	1.4e-46			57.96	HLA-DRI CLASS II HISTOCOMPATIBILITY PROTEIN; CHAIN: A, B, D, E, G, H, I, K; HLA-A2; CHAIN: C, F, I, L;	COMPLEX (MHC PROTEIN/ANTIGEN) DRA, DRB1 01010; COMPLEX (MHC PROTEIN/ANTIGEN), HISTOCOMPATIBILITY ANTIGEN
986	1aqp	B	45	201	1.4e-46	-0.34	0.58		HLA-DRI CLASS II HISTOCOMPATIBILITY PROTEIN; CHAIN: A, B, D, E, G, H, I, K; HLA-A2; CHAIN: C, F, I, L;	COMPLEX (MHC PROTEIN/ANTIGEN) DRA, DRB1 01010; COMPLEX (MHC PROTEIN/ANTIGEN), HISTOCOMPATIBILITY ANTIGEN
986	1lox2	A	22	202	8.5e-61			95.88	HLA-DR2; CHAIN: A, D; HLA-DR2; CHAIN: B, E; HLA-DR2; CHAIN: C, F;	IMMUNE SYSTEM HLA-DR2, MYELIN BASIC PROTEIN, MULTIPLE SCLEROSIS, 2 AUTOIMMUNITY, IMMUNE SYSTEM
986	1lox2	A	28	202	8.5e-61	-0.11	0.58		HLA-DR2; CHAIN: A, D; HLA-	IMMUNE SYSTEM HLA-DR2,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Bias	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									DR2; CHAIN: B, E; HLA-DR2; CHAIN: C, F;	MYELIN BASIC PROTEIN, MULTIPLE SCLEROSIS, 2 AUTOIMMUNITY, IMMUNE SYSTEM
986	1bx2	B	20	204	1.7e-45			59.12	HLA-DR2; CHAIN: A, D; HLA-DR2; CHAIN: B, E; HLA-DR2; CHAIN: C, F;	IMMUNE SYSTEM HLA-DR2, MYELIN BASIC PROTEIN, MULTIPLE SCLEROSIS, 2 AUTOIMMUNITY, IMMUNE SYSTEM
986	1bx2	B	45	201	1.7e-45	-0.39	0.46		HLA-DR2; CHAIN: A, D; HLA-DR2; CHAIN: B, E; HLA-DR2; CHAIN: C, F;	IMMUNE SYSTEM HLA-DR2, MYELIN BASIC PROTEIN, MULTIPLE SCLEROSIS, 2 AUTOIMMUNITY, IMMUNE SYSTEM
986	1fv1	A	29	202	3.4e-60	-0.31	0.90		MAJOR HISTOCOMPATIBILITY COMPLEX ALPHA CHAIN; CHAIN: A, D; MAJOR HISTOCOMPATIBILITY COMPLEX BETA CHAIN; CHAIN: B, E; MYELIN BASIC PROTEIN; CHAIN: C, F;	IMMUNE SYSTEM MHC CLASS II DR2A
986	1fv1	B	29	201	1.7e-46	-0.50	0.39		MAJOR HISTOCOMPATIBILITY COMPLEX ALPHA CHAIN; CHAIN: A, D; MAJOR HISTOCOMPATIBILITY COMPLEX BETA CHAIN; CHAIN: B, E; MYELIN BASIC PROTEIN; CHAIN: C, F;	IMMUNE SYSTEM MHC CLASS II DR2A
986	1hdm	A	20	207	3.4e-43			282.05	CLASS II HISTOCOMPATIBILITY ANTIGEN, M ALPHA CHAIN; A; CLASS II HISTOCOMPATIBILITY ANTIGEN, M BETA CHAIN; B; IMHC CLASS II I-AK; CHAIN: A, B, F; HEN EGG WHITE LYSOZYME PEPTIDE	IMMUNE SYSTEM RING6, HLA-DMA; RING7, HLA-DMB; HISTOCOMPATIBILITY PROTEIN, IMMUNE SYSTEM
986	1hak	A	20	202	1e-61			106.84		HISTOCOMPATIBILITY ANTIGEN I-AK HISTOCOMPATIBILITY ANTIGEN, MHC, PEPTIDE COMPLEX

SEQ NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
986	1iak	A	37	202	1e-61	-0.12	1.00		MHC CLASS II I-AK; CHAIN: A, B, P; HEN EGGWHITE LYSOZYME PEPTIDE	HISTOCOMPATIBILITY ANTIGEN I-AK HISTOCOMPATIBILITY ANTIGEN, MHC, PEPTIDE COMPLEX
986	1iak	B	23	201	1.5e-43			59.46	MHC CLASS II I-AK; CHAIN: A, B, P; HEN EGGWHITE LYSOZYME PEPTIDE	HISTOCOMPATIBILITY ANTIGEN I-AK HISTOCOMPATIBILITY ANTIGEN, MHC, PEPTIDE COMPLEX
986	1iao	B	1	201	1.2e-43			58.50	MHC CLASS II I-AD; CHAIN: A, B	MHC II MHC II, CLASS II MHC, I-A ₃ OVALBUMIN PEPTIDE
986	1iea	A	21	203	5.1e-59			100.86	MHC CLASS II I-EK; CHAIN: A, B, C, D ₂	HISTOCOMPATIBILITY ANTIGEN HISTOCOMPATIBILITY ANTIGEN
986	1iea	A	27	203	5.1e-59	-0.28	0.95		MHC CLASS II I-EK; CHAIN: A, B, C, D ₂	HISTOCOMPATIBILITY ANTIGEN HISTOCOMPATIBILITY ANTIGEN
986	1ieb	B	2	199	3.4e-45			53.16	MHC CLASS II I-EK; CHAIN: A, B, C, D ₂	HISTOCOMPATIBILITY ANTIGEN HISTOCOMPATIBILITY ANTIGEN
986	1ieb	B	1	199	3.4e-45			58.75	MHC CLASS II I-EK; CHAIN: A, B, C, D ₂	HISTOCOMPATIBILITY ANTIGEN HISTOCOMPATIBILITY ANTIGEN
986	1ieb	B	51	199	3.4e-45	-0.34	0.21		MHC CLASS II I-EK; CHAIN: A, B, C, D ₂	HISTOCOMPATIBILITY ANTIGEN HISTOCOMPATIBILITY ANTIGEN
986	2iad	A	20	207	3.4e-61			109.34	MHC CLASS II I-AD; CHAIN: A, B	MHC II MHC II, CLASS II MHC I-AD
986	2iad	A	37	206	3.4e-61	0.09	1.00		MHC CLASS II I-AD; CHAIN: A, B	MHC II MHC II, CLASS II MHC I-AD
986	2iad	B	2	201	3.4e-44			59.80	MHC CLASS II I-AD; CHAIN: A, B	MHC II MHC II, CLASS II MHC I-AD
987	1ady	A	52	214	1.9e-11	-0.45	0.60		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPTOPE MAPPING, LEUCINE-RICH 3 REPEATS
987	1a9n	A	49	130	3.8e-15	-0.29	0.89		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A; CHAIN: A, C; U2 B ⁺ ; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Bias	Verify score	PMF score	SEQOL D score	Compound	PDB annotation
987	1a9n	A	52	199	3.8e-14	0.10	0.40		U2 RNA HAIRPIN IV; CHAIN: Q; R; U2 A'; CHAIN: A, C; U2 B'; CHAIN: B, D;	SNRNP RIBONUCLEOPROTEIN COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA, RNA, SNRNP RIBONUCLEOPROTEIN)
987	1a9n	C	49	145	3.8e-15	0.07	0.94		U2 RNA HAIRPIN IV; CHAIN: Q; R; U2 A'; CHAIN: A, C; U2 B'; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA, RNA, SNRNP RIBONUCLEOPROTEIN)
987	1a9n	C	52	199	5.7e-14	0.05	0.35		U2 RNA HAIRPIN IV; CHAIN: Q; R; U2 A'; CHAIN: A, C; U2 B'; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA, RNA, SNRNP RIBONUCLEOPROTEIN)
987	1c1g	A	231	493	5.1e-19	-0.72	0.03		TROPOMYOSIN; CHAIN: A, B, C, D	CONTRACTILE PROTEIN TROPOMYOSIN COILED-COIL ALPHA-HELICAL, CONTRACTILE PROTEIN
987	1a0h	A	5	162	1.2e-18	0.33	0.98		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT; CALCIUM BINDING, CELL ADHESION
987	1dce	A	34	151	1.2e-14	0.27	0.66		RAB GERANYLGERANYLTRANSFERASE RASE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRANSFERASE BETA SUBUNIT; CHAIN: B, D;	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION; N-FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
987	1a89	A	48	150	1e-14	-0.19	0.52		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE RICH REPEAT; BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA
987	1a89	A	50	155	3.8e-15	-0.08	0.55		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE RICH REPEAT; BETA-BETA-ALPHA CYLINDER, DYNEIN, 2

SEQ NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fsi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
987	1qpu	A	236	491	7.6e-07			72.54	HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CHLAMYDOMONAS FLAGELLA CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL
987	1yrg	A	57	210	1.9e-12	-0.14	0.13		GTPASE-ACTIVATING PROTEIN RNA1_SCHPO; CHAIN: A, B;	CONTRACTILE PROTEIN TRANSCRIPTION RNAI P; RANGAP; GTPASE-ACTIVATING PROTEIN FOR SPI1, GTPASE-ACTIVATING PROTEIN, GAP, RNAI P, RANGAP, LRR, LEUCINE-2 RICH REPEAT PROTEIN, TWINNING, HEMIHEDRAL TWINNING, 3 MEROHEDRAL TWINNING, MEROHEDRY
991	1qf8	A	7	123	3.8e-56	0.46	1.00		CASEIN KINASE II; CHAIN: A, B;	TRANSFERASE CASEIN KINASE BETA SUBUNIT (1-182), SER/THR
991	1qf8	A	7	123	6.8e-51	0.46	1.00		CASEIN KINASE II; CHAIN: A, B;	PROTEIN KINASE, 2 ZN FINGER
993	2oc	H	73	141	8.5e-29	0.10	0.07		CYTOCHROME C OXIDASE; CHAIN: A, B, C, D, E, F, G, H, I, J, K, L, M, N, O, P, Q;	TRANSFERASE CASEIN KINASE BETA SUBUNIT (1-182), SER/THR
										OXIDOREDUCTASE FERROCYTOCHROME C OXYGEN OXIDOREDUCTASE; OXIDOREDUCTASE, CYTOCHROME(C)-OXYGEN, CYTOCHROME C2 OXIDASE
994	1ddq	C	1	1076	0	-0.22	0.96		DNA-DIRECTED RNA POLYMERASE; CHAIN: A, B; DNA-DIRECTED RNA POLYMERASE; CHAIN: C; DNA-DIRECTED RNA POLYMERASE; CHAIN: D; DNA-DIRECTED	TRANSFERASE, TRANSCRIPTION, DNA-DIRECTED RNA POLYMERASE, 3D-2 STRUCTURE

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									RNA POLYMERASE, CHAIN: E;	
995	1hor		2	50	1.4e-08	-0.39	0.05		TRANSCRIPTION FACTOR PML; CHAIN: NULL;	TRANSCRIPTION REGULATION PROTO-ONCOGENE, NUCLEAR BODIES (POBS); LEUKEMIA, 2 TRANSCRIPTION REGULATION
995	1che		10	51	1.7e-12	0.29	0.59		VIRUS EQUINE HERPES VIRUS-1 (C3HC4, OR RING DOMAIN) 1C1C 3 (NMR, 1 STRUCTURE) 1C1C 4	
995	1che		6	60	5.7e-12	-0.45	0.47		VIRUS EQUINE HERPES VIRUS-1 (C3HC4, OR RING DOMAIN) 1C1C 3 (NMR, 1 STRUCTURE) 1C1C 4	
995	1bw	A	10	51	5.1e-10	-0.04	0.52		SIGNAL TRANSDUCTION PROTEIN CBL; CHAIN: A; ZAP-70 PEPTIDE; CHAIN: B; UBIQUITIN-CONJUGATING ENZYME E12-18 KDA UBCH7; CHAIN: C;	LIGASE CBL; UBCH7; ZAP-70, E2, UBIQUITIN, E3, PHOSPHORYLATION, 2 TYROSINE KINASE, UBIQUITINATION, PROTEIN DEGRADATION,
995	1bw	A	9	60	3.8e-09	-0.46	0.30		SIGNAL TRANSDUCTION PROTEIN CBL; CHAIN: A; ZAP-70 PEPTIDE; CHAIN: B; UBIQUITIN-CONJUGATING ENZYME E12-18 KDA UBCH7; CHAIN: C;	LIGASE CBL; UBCH7; ZAP-70, E2, UBIQUITIN, E3, PHOSPHORYLATION, 2 TYROSINE KINASE, UBIQUITINATION, PROTEIN DEGRADATION,
995	1fw		98	134	3.4e-05	-0.11	0.03		NUCLEAR FACTOR XNF7; CHAIN: NULL;	ZINC-BINDING PROTEIN ZINC- BINDING PROTEIN, XNF7, BBOX, DEVELOPMENT; 3 MID-BLASTULA- TRANSITION
995	1g25	A	6	57	0.00017	-0.33	0.46		CDK-ACTIVATING KINASE ASSEMBLY FACTOR MAT1; CHAIN: A;	METAL BINDING PROTEIN RING FINGER PROTEIN MAT1; RING FINGER (C3HC4)
995	1rmd		4	100	1.1e-16	0.13	0.49		RAG1; CHAIN: NULL;	DNA-BINDING PROTEIN V(D)J

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										RECOMBINATION ACTIVATING PROTEIN 1; RAG1, VDJ RECOMBINATION ANTIBODY, MAD RING FINGER, 2 ZINC BINDING PROTEIN, 2 ZINC FINGER, DNA-BINDING PROTEIN
996	1am9	B	277	345	7.6e-09	-0.25	0.01		STEROL REGULATORY ELEMENT BINDING PROTEIN 1A; CHAIN: A, B, C, D; DNA; CHAIN: E, F, G, H;	COMPLEX (TRANSCRIPTION REGULATION/DNA) SREBP-1A; STEROL REGULATORY ELEMENT BINDING PROTEIN; 2 BASIC-HELIX-LOOP-HELIX-LEUCINE ZIPPER, SREBP, TRANSCRIPTION 3 FACTOR, COMPLEX (TRANSCRIPTION REGULATION/DNA)
996	1am2	A	277	354	3.8e-15	-0.60	0.01		MAX PROTEIN; CHAIN: A, C; DNA; CHAIN: B, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) MYN PROTEIN; MAX, DNA BINDING, BASIC-HELIX-LOOP-HELIX-LEUCINE ZIPPER, 2 TRANSCRIPTION FACTOR, COMPLEX (DNA-BINDING PROTEIN/DNA)
996	1h1o	A	268	343	1.9e-13	-0.26	0.10		TRANSCRIPTION FACTOR MAX; CHAIN: A, B; DNA (5'-D'C'CP*AP*CP*CP*AP*CP*GP*TP*GP*GP*TP)-3'; CHAIN: C, D;	COMPLEX (TRANSCRIPTION FACTOR MAX/DNA) TRANSCRIPTIONAL REGULATION, DNA BINDING, COMPLEX 2 (TRANSCRIPTION FACTOR MAX/DNA)
996	1h1o	B	277	343	1.9e-12	-0.32	0.19		TRANSCRIPTION FACTOR MAX; CHAIN: A, B; DNA (5'-D'C'CP*AP*CP*CP*AP*CP*GP*TP*GP*GP*TP)-3'; CHAIN: C, D;	COMPLEX (TRANSCRIPTION FACTOR MAX/DNA) TRANSCRIPTIONAL REGULATION, DNA BINDING, COMPLEX 2 (TRANSCRIPTION FACTOR MAX/DNA)

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
997	1byu	A	17	139	5.1e-46	-0.02	0.64		GTP-BINDING PROTEIN RAN; CHAIN: A, B;	TRANSPORT PROTEIN TC4; GTPASE, NUCLEAR TRANSPORT, TRANSPORT PROTEIN
997	1byu	B	13	139	1.2e-46	0.17	0.72		GTP-BINDING PROTEIN RAN; CHAIN: A, B;	TRANSPORT PROTEIN TC4; GTPASE, NUCLEAR TRANSPORT, TRANSPORT PROTEIN
997	1cc0	A	23	140	3.4e-47	-0.23	0.96		TRANSFORMING PROTEIN RHOA; CHAIN: A, C, RHO GDP DISSOCIATION INHIBITOR ALPHA; CHAIN: E, F;	SIGNALING PROTEIN GTP-BINDING PROTEIN RHOA, GTPASE RHOA; RHO GDI 1; RHO GTPASE, G-PROTEIN, SIGNALING PROTEIN
997	1csz	A	23	140	1e-47	-0.14	0.98		HIS-TAGGED TRANSFORMING PROTEIN RHOA(0-181); CHAIN: A; PCS; CHAIN: B;	SIGNALING PROTEIN PROTEIN-PROTEIN COMPLEX, ANTIPARALLEL COILED-COIL
997	1d5c	A	22	143	1.4e-49	0.14	0.84		RAB6 GTPASE; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS G-PROTEIN, GTPASE, RAB6, VESICULAR TRAFFICKING
997	1d56	A	22	140	8.5e-49	-0.05	0.88		RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 2; CHAIN: A; RHO GDP-DISSOCIATION INHIBITOR 2; CHAIN: B;	SIGNALING PROTEIN P21-RAC2; RHO GDI 2, RHO-GDI BETA, LY-GDI; BETA SANDWICH, PROTEIN-PROTEIN COMPLEX, G-DOMAIN, 2 IMMUNOGLOBULIN FOLD, WALKER FOLD, GTP-BINDING PROTEIN
997	1lbr	A	20	145	1.4e-45		68.78		RAN; CHAIN: A, C; IMPORTIN BETA SUBUNIT; CHAIN: B, D;	SMALL GTPASE KARYOPHERIN BETA, P04 SMALL GTPASE, NUCLEAR TRANSPORT RECEPTOR
997	1mh1		17	145	5.1e-50		52.24		RAC1; CHAIN: NULL;	GTP-BINDING GTP-BINDING, GTPASE, SMALL G-PROTEIN, RHO FAMILY, RAS SUPER 2 FAMILY
997	1mh1		22	140	5.1e-50	-0.12	0.87		RAC1; CHAIN: NULL;	GTP-BINDING GTP-BINDING, GTPASE, SMALL G-PROTEIN, RHO FAMILY, RAS SUPER 2 FAMILY
997	1lrp	C	19	145	1.4e-45			65.13	RAN; CHAIN: A, C; NUCLEAR	COMPLEX (SMALL)

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	FMF score	SEQOL D score	Compound	PDB annotation
									PORE COMPLEX PROTEIN NUP348; CHAIN: B; D;	GTPASE/NUCLEAR PROTEIN) COMPLEX (SMALL GTPASE/NUCLEAR PROTEIN), SMALL GTPASE, 2 NUCLEAR TRANSPORT
997	1zbd	A	17	144	1.7e-53			54.15	RAB-3A; CHAIN: A; RABPHILIN-3A; CHAIN: B;	COMPLEX (GTP-BINDING/EFFECTOR) RAS-RELATED PROTEIN RAB3A; COMPLEX (GTP-BINDING/EFFECTOR), G PROTEIN, EFFECTOR, RABCDR, 2 SYNAPTIC EXOCYTOSIS, RAB PROTEIN, RAB3A, RABPHILIN
997	1zbd	A	18	143	1.7e-53	0.17	0.78		RAB-3A; CHAIN: A; RABPHILIN-3A; CHAIN: B;	COMPLEX (GTP-BINDING/EFFECTOR) RAS-RELATED PROTEIN RAB3A; COMPLEX (GTP-BINDING/EFFECTOR), G PROTEIN, EFFECTOR, RABCDR, 2 SYNAPTIC EXOCYTOSIS, RAB PROTEIN, RAB3A, RABPHILIN
997	2tgr	A	22	141	3.4e-46	-0.07	0.89		GTP BINDING PROTEIN (G25K); CHAIN: A; GTPASE ACTIVATING PROTEIN (RHG); CHAIN: B;	HYDROLASE CDC42/CDC42GAP; CDC42/CDC42GAP; TRANSITION STATE, G-PROTEIN, GAP, CDC42, ALF3, HYDROLASE
997	3rab	A	17	143	5.1e-55	0.19	0.88		RAB3A; CHAIN: A;	HYDROLASE G PROTEIN, VESICULAR TRAFFICKING, GTP HYDROLYSIS, RAB 2 PROTEIN, NEUROTRANSMITTER RELEASE, HYDROLASE
997	3rab	A	17	145	5.1e-55			64.11	RAB3A; CHAIN: A;	HYDROLASE G PROTEIN, VESICULAR TRAFFICKING, GTP HYDROLYSIS, RAB 2 PROTEIN, NEUROTRANSMITTER RELEASE, HYDROLASE

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
998	1a06		1	174	1.7e-50	-0.20	0.16		CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE; CHAIN: NULL;	KINASE KINASE SIGNAL TRANSDUCTION, CALCIUM/CALMODULIN
998	1apm	E	1	175	5.1e-66	-0.21	0.53		TRANSFERASE(PHOSPHOTRANSFERASE) SC-/AMPS-DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (C/AFPKS) 1APM 3 (CATALYTIC SUBUNIT) ALPHA ISOENZYME MUTANT WITH SER 139 1APM 4 REPLACED BY ALA (S139AS) COMPLEX WITH THE PEPTIDE 1APM 5 INHIBITOR PKI(5-24) AND THE DETERGENT MEGA-8 1APM 6	
998	1cmk	E	1	175	5.1e-66	-0.17	0.47		PHOSPHOTRANSFERASE CAMP-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT 1CMK 3 (E.C.2.7.1.37) 1CMK 4	
998	1cnp	E	1	161	1.2e-60	-0.02	0.78		TRANSFERASE(PHOSPHOTRANSFERASE) CAMP-DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (C/AFK) 1CTP 3 (CATALYTIC SUBUNIT) 1CTP 4	
998	1fem	C	1	160	3.4e-53	-0.02	0.51		SERINE/THREONINE-PROTEIN KINASE PAK-ALPHA; CHAIN: A, B; SERINE/THREONINE-PROTEIN KINASE PAK-ALPHA; CHAIN: C, D;	TRANSFERASE KINASE DOMAIN, AUTOINHIBITORY FRAGMENT, HOMODIMER
998	1lcm		1	169	1.2e-38	-0.02	0.37		TWITCHIN; CHAIN: NULL;	KINASE KINASE TWITCHIN, INTRASTERIC REGULATION
998	1kob	A	1	169	1.2e-40	-0.02	0.72		TWITCHIN; CHAIN: A, B;	KINASE KINASE TWITCHIN, INTRASTERIC REGULATION
998	1phk		1	140	3.4e-54	0.13	0.80		PHOSPHORYLASE KINASE; CHAIN: NULL;	KINASE RABBIT MUSCLE PHOSPHORYLASE KINASE;

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
										GLYCOGEN METABOLISM, TRANSFERASE, SERINE/THREONINE-PROTEIN, 2 KINASE, ATP-BINDING, CALMODULIN-BINDING
998	1tki	A	1	149	1.7e-34	0.18	0.75		TITIN; CHAIN: A, B;	SERINE KINASE SERINE KINASE, TITIN, MUSCLE, AUTOINHIBITION
998	1tki	A	1	186	1.9e-34	-0.12	0.25		TITIN; CHAIN: A, B;	SERINE KINASE SERINE KINASE, TITIN, MUSCLE, AUTOINHIBITION
1000	1b1h	A	10	283	1.7e-27	0.28	0.40		HEMOLIN; CHAIN: A, B;	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION
1000	1cs6	A	29	283	3.4e-34	0.09	0.10		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
1000	1evs	C	21	199	3.4e-25	0.08	0.15		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1000	1evs	D	112	284	5.1e-36	0.15	0.21		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1000	1evs	D	21	199	1.2e-26	0.03	-0.03		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1000	1epf	A	123	282	3.4e-18	0.11	-0.13		NEURAL CELL ADHESION	CELL ADHESION NCAM; NCAM;

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1000	1epf	A	33	201	3.4e-24	0.11	-0.09		MOLECULE; CHAIN: A, B, C, D;	IMMUNOGLOBULIN FOLD, GLYCOPROTEIN
1000	1l2q	A	117	281	1.7e-19	0.12	0.31		NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	CELL ADHESION; NCAM; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN
1000	1l2q	A	28	208	3.4e-28	0.00	0.22		HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN; A;	IMMUNE SYSTEM FC-EPSILON RI-ALPHA; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN
1000	1f6a	A	116	281	1e-17	0.31	0.57		HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN; A;	IMMUNE SYSTEM FC-EPSILON RI-ALPHA; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN
1000	1f6a	A	26	207	1.4e-27	-0.04	0.12		HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN; A; IG EPSILON CHAIN C REGION; CHAIN: B, D;	IMMUNE SYSTEM HIGH AFFINITY IGE-FC RECEPTOR, FC(EPSILON) IGE-FC; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN, IGE ANTIBODY, IGE-FC
1000	1f6g	A	115	281	1.7e-19	0.15	-0.12		FC RECEPTOR FC(GAMMA)RIIA; CHAIN: A;	IMMUNE SYSTEM, MEMBRANE PROTEIN CD32; FC RECEPTOR, IMMUNOGLOBULIN, LEUKOCYTE, CD32
1000	1f6g	A	26	205	5.1e-29	0.23	0.41		FC RECEPTOR FC(GAMMA)RIIA; CHAIN: A;	IMMUNE SYSTEM, MEMBRANE PROTEIN CD32; FC RECEPTOR, IMMUNOGLOBULIN, LEUKOCYTE, CD32
1000	1f6l	A	114	281	3.4e-17	0.05	0.06		LOW AFFINITY	IMMUNE SYSTEM RECEPTOR BETA

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									IMMUNOGLOBULIN GAMMA FC REGION CHAIN: A;	SANDWICH, IMMUNOGLOBULIN-LIKE, RECEPTOR
1000	1fin	A	24	206	1.3e-24	0.07	0.58		LOW AFFINITY IMMUNOGLOBULIN GAMMA FC REGION CHAIN: A;	IMMUNE SYSTEM RECEPTOR BETA LIKE, RECEPTOR
1000	1kxa		207	284	5.1e-12	0.35	0.33		TWITCHIN; CHAIN: NULL;	KINASE KINASE, TWITCHIN, INTRASTERIC REGULATION
1000	1nct		213	284	3.4e-13	0.47	-0.15		TITIN; CHAIN: NULL;	MUSCLE PROTEIN CONNECTIN, NEXTMS; CELL ADHESION, GLYCOPROTEIN, TRANSMEMBRANE, REPEAT, BRAIN, 2 IMMUNOGLOBULIN FOLD, ALTERNATIVE SPLICING, SIGNAL, 3 MUSCLE PROTEIN
1000	1nkr		117	282	3.4e-29	0.20	0.76		P58-CL42 KIR; CHAIN: NULL;	INHIBITORY RECEPTOR KILLER CELL, INHIBITORY RECEPTOR, KILLER CELLS, IMMUNOLOGICAL 2 RECEPTORS, IMMUNOGLOBULIN FOLD
1000	1nkr		12	113	6.8e-13	-0.51	0.22		P58-CL42 KIR; CHAIN: NULL;	INHIBITORY RECEPTOR KILLER CELL, INHIBITORY RECEPTOR, KILLER CELLS, IMMUNOLOGICAL 2 RECEPTORS, IMMUNOGLOBULIN FOLD
1000	1nkr		27	216	1e-30			71.59	P58-CL42 KIR; CHAIN: NULL;	INHIBITORY RECEPTOR KILLER CELL, INHIBITORY RECEPTOR, KILLER CELLS, IMMUNOLOGICAL 2 RECEPTORS, IMMUNOGLOBULIN FOLD
1000	1nkr		28	204	1e-30	0.22	0.87		P58-CL42 KIR; CHAIN: NULL;	INHIBITORY RECEPTOR KILLER CELL, INHIBITORY RECEPTOR;

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										INHIBITORY RECEPTOR, NATURAL KILLER CELLS, IMMUNOLOGICAL 2 RECEPTORS, IMMUNOGLOBULIN FOLD
1000	1tmn		213	284	3.4e-13	0.37	-0.18		MUSCLE PROTEIN TITIN MODULE M3 (CONNECTIN) ITNM 3 (NMR, MINIMIZED AVERAGE STRUCTURE) ITNM 4 ITNM 58	
1000	1yah	H	28	236	8.5e-07			34.09	FAB FRAGMENT; CHAIN: NULL;	IMMUNOGLOBULIN ANTI- NITROPHENOL, LAMBDA LIGHT CHAIN, IMMUNOGLOBULIN
1000	2dli	A	117	282	3.4e-29	0.22	0.51		MHC CLASS I NK CELL RECEPTOR PRECURSOR; CHAIN: A;	IMMUNE SYSTEM P58 NATURAL KILLER CELL RECEPTOR; KIR, NATURAL KILLER RECEPTOR, INHIBITORY RECEPTOR, 2 IMMUNOGLOBULIN
1000	2dli	A	26	203	5.1e-29	0.23	0.74		MHC CLASS I NK CELL RECEPTOR PRECURSOR; CHAIN: A;	IMMUNE SYSTEM P58 NATURAL KILLER CELL RECEPTOR; KIR, NATURAL KILLER RECEPTOR, INHIBITORY RECEPTOR, 2 IMMUNOGLOBULIN
1000	2fcb	A	115	281	5.1e-20	0.26	-0.08		FC GAMMA RIIB; CHAIN: A;	IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32, IMMUNE SYSTEM
1000	2fcb	A	26	206	3.4e-29	0.03	0.35		FC GAMMA RIIB; CHAIN: A;	IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32, IMMUNE SYSTEM
1001	1d5r	A	291	344	0.0019	-0.64	0.07		PHOSPHONOSITIDE PHOSPHOTASE PTEN; CHAIN: A;	HYDROLASE C2 DOMAIN, PHOSPHOTIDYLINOSITOL, PHOSPHOTASE, HYDROLASE
1003	1d5r	A	209	262	0.0019	-0.64	0.07		PHOSPHONOSITIDE PHOSPHOTASE PTEN; CHAIN: A;	HYDROLASE C2 DOMAIN, PHOSPHOTIDYLINOSITOL, PHOSPHOTASE, HYDROLASE

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1004	1d5r	A	291	344	0.0019	-0.64	0.07		PHOSPHONOSITIDE PHOSPHOTASE P1EN; CHAIN: A;	HYDROLASE C2 DOMAIN, PHOSPHODIYLYNOSITOL PHOSPHATASE, HYDROLASE
1010	1cun	A	164	396	5.7e-16	0.04	-0.03		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1010	1cun	A	213	429	1.5e-16	-0.08	0.13		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1010	1cun	A	293	505	1.7e-13	-0.12	0.23		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1010	1dn1	B	236	470	5.7e-18	-0.32	0.01		SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1A; CHAIN: B;	ENDOCYTOSIS/EXOCYTOSIS NSEC1; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT
1010	1eer	A	61	288	0.0013	-0.61	0.00		REPLICATION TERMINATOR PROTEIN; CHAIN: A; DNA 16MER DUPLEX REPLICATION TERMINATOR; CHAIN: B, C;	COMPLEX (DNA-BINDING PROTEIN/DNA) TLS; TER; DNA-BINDING, DNA REPLICATION, 2 COMPLEX (DNA-BINDING PROTEIN/DNA)
1010	1f6o	A	133	329	3.8e-11	0.00	0.00		SSO1 PROTEIN; CHAIN: A;	MEMBRANE PROTEIN FOUR HELIX BUNDLE, ALPHA HELIX
1010	1f6o	A	217	401	7.6e-11	0.02	-0.12		SSO1 PROTEIN; CHAIN: A;	MEMBRANE PROTEIN FOUR HELIX BUNDLE, ALPHA HELIX
1010	1quu	A	75	370	1.1e-22	-0.31	0.05		HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										CONTRACTILE PROTEIN
1013	1dhn	A	109	138	1.1e-12			59.97	DEFENSIN DEFENSIN /HNPS-3 IDFN 3	
1013	1dfn	A	110	138	1.1e-12	-0.35	1.00		DEFENSIN DEFENSIN /HNPS-3 IDFN 3	
1013	1dhn	A	110	138	3.4e-11	-0.35	1.00		DEFENSIN DEFENSIN /HNPS-3 IDFN 3	
1014	1cili		14	636	5.7e-59			148.75	COLICIN IA; CHAIN: NULL;	TRANSMEMBRANE PROTEIN COLICIN, BACTERIOCIN, ION CHANNEL FORMATION, TRANSMEMBRANE 2 PROTEIN
1014	1cum	A	190	394	3.8e-15	0.12	-0.09		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2,2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1014	1cum	A	218	447	1.9e-15	0.06	0.17		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2,2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1014	1cum	A	345	583	3.8e-21	0.11	0.04		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2,2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1014	1cum	A	419	634	1.9e-19	0.44	-0.02		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2,2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1014	1cum	A	50	284	1.9e-09	-0.09	0.30		ALPHA SPECTRIN; CHAIN: A;	STRUCTURAL PROTEIN TWO

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									B, C;	REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1014	1cm	A	525	741	5.7e-10	-0.06	0.12		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1014	1dg3	A	55	307	0.0057	-0.16	0.17		INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 1; CHAIN: A;	SIGNALING PROTEIN GUANINE NUCLEOTIDE- BINDING PROTEIN 1; GBP, GTP HYDROLYSIS, GDP, GMP, INTERFERON INDUCED, DYNAMIN 2 RELATED, LARGE GTPASE FAMILY, SIGNALING PROTEIN
1014	1dm1	B	297	509	1.5e-18	0.07	-0.07		SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1A; CHAIN: B;	ENDOCYTOSIS/EXOCYTOSIS NSEC1; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT
1014	1dm1	B	370	598	5.7e-26	-0.04	0.23		SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1A; CHAIN: B;	ENDOCYTOSIS/EXOCYTOSIS NSEC1; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT
1014	1dm1	B	484	733	1.7e-09	0.02	0.66		SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1A; CHAIN: B;	ENDOCYTOSIS/EXOCYTOSIS NSEC1; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT
1014	1fio	A	361	518	1.9e-11	0.01	-0.17		SSO1 PROTEIN; CHAIN: A;	MEMBRANE PROTEIN FOUR HELIX BUNDLE, ALPHA HELIX
1014	1fkx	C	308	422	1.9e-05	0.08	0.01		PREFOLDIN; CHAIN: A; PREFOLDIN; CHAIN: B; PREFOLDIN; CHAIN: C;	CHAPERONE ARCHAEAAL PROTEIN
1014	1fkx	C	391	513	3.8e-07	0.00	0.15		PREFOLDIN; CHAIN: A; PREFOLDIN; CHAIN: B; PREFOLDIN; CHAIN: C;	CHAPERONE ARCHAEAAL PROTEIN
1014	1fkx	C	472	578	1.9e-05	0.26	0.22		PREFOLDIN; CHAIN: A; PREFOLDIN; CHAIN: B;	CHAPERONE ARCHAEAAL PROTEIN

SEQ NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1014	1fxk	C	552	635	0.00057	0.21	0.11		PREFOLDIN; CHAIN: C; PREFOLDIN; CHAIN: A; PREFOLDIN; CHAIN: B; PREFOLDIN; CHAIN: C; HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CHAPERONE ARCHAEAAL PROTEIN
1014	1quu	A	272	549	1.1e-24	0.15	0.07		HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL
1014	1quu	A	321	580	1.3e-32	0.48	0.01		HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL
1014	1quu	A	359	630	7.6e-27	0.20	0.15		HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL
1014	1quu	A	471	746	3.8e-17	-0.05	0.03		HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL
1014	1quu	A	81	398	3.8e-15	-0.06	0.03		HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL
1015	1alh	A	349	429	1.2e-23	-0.31	0.62		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1015	1alh	A	378	468	1.7e-24	0.01	-0.06		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1015	1alh	A	405	498	1.7e-26	0.11	0.03		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1015	1alh	A	472	555	1e-27	-0.37	0.28		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA),

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fsi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1015	1ath	A	901	981	3.4e-30	0.34	0.10		OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	ZINC FINGER, DNA-BINDING PROTEIN
1015	1ath	A	929	1010	3.4e-30	0.10	0.87		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1015	1bbo		505	554	1.7e-10	-0.65	0.18		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
									DNA-BINDING PROTEIN HUMAN ENHANCER-BINDING PROTEIN MBP-1 MUTANT WITH CYS 11 1BBO.3 REPLACED BY ASU (C11ABU) (NMR, 60 STRUCTURES) 1BBO 4	
1015	1mey	C	349	429	1.7e-41	-0.12	0.81		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1015	1mey	C	374	468	1.7e-42	-0.01	0.72		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1015	1mey	C	404	496	1.7e-45	-0.01	0.82		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1015	1mey	C	443	527	5.1e-47	-0.25	0.95		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA

SEQ NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									PROTEIN; CHAIN: C, F, G;	INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1015	1mey	C	471	556	3.4e-46	-0.26	0.90		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1015	1mey	C	530	612	1.5e-36	0.01	-0.14		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1015	1mey	C	698	778	6.8e-44	0.02	-0.20		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1015	1mey	C	840	953	5.1e-45	0.12	-0.15		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1015	1mey	C	901	981	3.4e-50	0.25	0.51		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1015	1mey	C	928	1010	3.4e-50	-0.07	0.88		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1015	1mey	G	500	527	3.4e-12	-0.05	0.39		DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1015	1mey	G	528	556	5.1e-11	-0.71	0.24		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1015	1mey	G	839	865	1.5e-11	0.22	-0.18		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1015	1mey	G	926	953	1e-12	-0.03	0.42		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1015	1mey	G	942	1010	8.5e-12	0.23	0.65		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1015	1paa		985	1013	1.7e-05	-0.38	0.96		TRANSCRIPTION REGULATION FACTOR ADRI (RESIDUES 130-159) IPAA 3 (PAPA - CARBOXY TERMINAL ZINC FINGER DOMAIN) MUTANT WITH IPAA 4 PRO 131 REPLACED BY ALA, PRO 133 REPLACED BY ALA, CYS 140 IPAA 5 REPLACED BY ALA (P131A,P133A,C140A)	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1015	1sp1		985	1010	0.00051	-0.10	0.70		(NMR, 10 STRUCTURES) IPAA 6 SP IF3; CHAIN: NULL;	ZINC FINGER TRANSCRIPTION FACTOR SP1; ZINC FINGER, TRANSCRIPTION ACTIVATION, SP1
1015	1sp2		349	375	0.00017	-0.77	0.27		SP IF2; CHAIN: NULL;	ZINC FINGER TRANSCRIPTION FACTOR SP1; ZINC FINGER, TRANSCRIPTION ACTIVATION, SP1
1015	1sp2		985	1010	1.9e-05	-0.54	0.90		SP IF2; CHAIN: NULL;	ZINC FINGER TRANSCRIPTION FACTOR SP1; ZINC FINGER, TRANSCRIPTION ACTIVATION, SP1
1015	1tf3	A	377	468	6.8e-17	-0.11	0.05		TRANSCRIPTION FACTOR IIIA; CHAIN: A; 5S RNA GENE; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) TFIIIA; 5S GENE; NMR, TFIIIA, PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA 2 GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCRIPTION REGULATION/DNA)
1015	1tf3	A	405	496	3.4e-18	0.15	0.23		TRANSCRIPTION FACTOR IIIA; CHAIN: A; 5S RNA GENE; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) TFIIIA; 5S GENE; NMR, TFIIIA, PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA 2 GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCRIPTION REGULATION/DNA)
1015	1tf3	A	472	551	1.7e-18	-0.17	0.03		TRANSCRIPTION FACTOR IIIA; CHAIN: A; 5S RNA GENE; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) TFIIIA; 5S GENE; NMR, TFIIIA, PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA 2 GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCRIPTION REGULATION/DNA)

SEQ ID NO:	PDB ID	CITAI N ID	STAR T AA	END AA	Fsi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1015	1th3	A	929	1010	1.5e-21	-0.17	0.64		TRANSCRIPTION FACTOR IIIA; CHAIN: A; 5S RNA GENE; CHAIN: E; F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) TFIIIA; 5S GENE; NMR, TFIIIA PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA 2 GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCRIPTION REGULATION/DNA)
1015	1th6	A	405	565	8.5e-34	-0.42	0.47		TFIIIA; CHAIN: A; D; 5S RIBOSOMAL RNA GENE; CHAIN: B; C; E; F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2
1015	1th6	A	472	593	1.7e-28	-0.65	0.00		TFIIIA; CHAIN: A; D; 5S RIBOSOMAL RNA GENE; CHAIN: B; C; E; F;	TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1015	1ubd	C	351	496	7.6e-17	-0.56	0.29		YY1; CHAIN: C; ADENOVIRUS P5 ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A; B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1015	1ubd	C	354	468	8.5e-31	-0.39	0.28		YY1; CHAIN: C; ADENOVIRUS P5 ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A; B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1015	1ubd	C	384	497	1.7e-31	-0.13	0.47		YY1; CHAIN: C; ADENOVIRUS P5 ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION; INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1015	1ubd	C	412	527	5.1e-30	-0.38	0.54		YY1; CHAIN: C; ADENOVIRUS P5 ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION; INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1015	1ubd	C	479	584	1e-31	-0.26	0.57		YY1; CHAIN: C; ADENOVIRUS P5 ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION; INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1015	1ubd	C	813	953	6.8e-28	0.04	-0.18		YY1; CHAIN: C; ADENOVIRUS P5 ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION; INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)

SEQ NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Fsi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1015	1ubd	C	848	981	3.4e-30	0.13	0.00		YY1; CHAIN: C; ADENOVIRUS P5 ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	(TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION; INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1015	1ubd	C	908	1006	3.4e-34	0.22	0.84		YY1; CHAIN: C; ADENOVIRUS P5 ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION; INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1015	1ubd	C	933	1086	5.1e-27	-0.56	0.81		YY1; CHAIN: C; ADENOVIRUS P5 ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION; INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1015	2adr		349	403	6.8e-12	-0.66	0.19		ADR1; CHAIN: NULL;	TRANSCRIPTION REGULATION; TRANSCRIPTION REGULATION, ADR1, ZINC FINGER, NMR
1015	2adr		503	558	8.5e-15	-0.80	0.39		ADR1; CHAIN: NULL;	TRANSCRIPTION REGULATION; TRANSCRIPTION REGULATION, ADR1, ZINC FINGER, NMR
1015	2adr		901	955	3.4e-16	0.39	0.09		ADR1; CHAIN: NULL;	TRANSCRIPTION REGULATION; TRANSCRIPTION REGULATION

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	PsI Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1015	2adr		957	1015	6.8e-18	-0.01	0.80		ADRI; CHAIN: NULL;	ADRI, ZINC FINGER, NMR TRANSCRIPTION REGULATION
1015	2drp	A	372	428	3.4e-06	-0.30	0.11		COMPLEX(TRANSCRIPTION REGULATION/DNA) TRAMTRACK PROTEIN (TWO ZINC-FINGER PEPTIDE) COMPLEXED WITH 2DRP 3 DNA 2DRP 4	ADRI, ZINC FINGER, NMR TRANSCRIPTION REGULATION
1015	2drp	A	501	556	8.5e-10	-0.47	0.01		COMPLEX(TRANSCRIPTION REGULATION/DNA) TRAMTRACK PROTEIN (TWO ZINC-FINGER PEPTIDE) COMPLEXED WITH 2DRP 3 DNA 2DRP 4	ADRI, ZINC FINGER, NMR TRANSCRIPTION REGULATION
1015	2gii	A	354	428	3.4e-18	-0.36	0.21		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C; D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1015	2gii	A	358	467	1.5e-26	-0.44	0.10		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C; D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1015	2gii	A	404	556	6.8e-33	-0.34	0.71		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C; D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1015	2gii	A	451	583	8.5e-33	-0.29	0.28		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C; D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1015	2gii	A	479	593	5.1e-28	-0.67	0.15		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C; D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Pst Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1015	2gji	A	901	1010	1e-33	-0.18	0.96		ZINC FINGER PROTEIN GLI; CHAIN: A; DNA; CHAIN: C, D;	GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA) COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1015	7znf		985	1013	3.4e-05	-0.23	0.31		ZINC FINGER DNA BINDING DOMAIN ZINC-FINGER (ZFY-SWAP) (NMR, 12 STRUCTURES) 7ZNF 3	
1021	2ccc	A	1	299	3.4e-88	0.01	-0.17		CYTOCHROME C OXIDASE; CHAIN: A, B, C, D, E, F, G, H, I, J, K, L, M, N, O, P, Q;	OXIDOREDUCTASE FERROCYTOCHROME C:OXYGEN OXIDOREDUCTASE; OXIDOREDUCTASE; CYTOCHROME(C)-OXYGEN, CYTOCHROME C 2 OXIDASE
1023	1anu	A	48	610	0			139.53	GRAMICIDIN SYNTHETASE 1; CHAIN: A, B; PHENYLALANINE; CHAIN: C, D;	PEPTIDE SYNTHETASE GRSA; PEPTIDE SYNTHETASE, GRSA, ADENYLATE FORMING
1023	1lei		59	608	0			133.28	LUCIFERASE; CHAIN: NULL;	OXIDOREDUCTASE OXIDOREDUCTASE, MONOOXYGENASE, PHOTOPROTEIN, LUMINESCENCE
1028	1alh	A	98	184	3.4e-29			76.54	QSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1028	1mcy	C	157	239	1.7e-50			97.35	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2

SEQ NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1028	1rf5	A	97	269	1.46-36			106.38	TH1A: CHAIN: A, D: 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE II, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT; YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)
1028	1ubd	C	130	239	6.8e-35			87.68	YY1: CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	INSECT IMMUNITY INSECT IMMUNITY, 1PS-BINDING, HOMOPHILIC ADHESION
1028	2gji	A	99	240	3.4e-31			87.54	ZINC FINGER PROTEIN GLI1; CHAIN: A, DNA; CHAIN: C, D;	COMPLEX (IMMUNOGLOBULIN/RECEPTOR) IMMUNOGLOBULIN FOLD, TRANSMEMBRANE,
1029	1bhh	A	1	351	6.8e-48			65.92	HEMOLIN; CHAIN: A, B;	
1029	1cap	B	133	348	1.7e-10			55.72	CATALYTIC ANTIHODY 17E8 COMPLEXED WITH PHENYL [1- (1-N, SUCCINYLAMINO)PENTYL] LEAP 3 PHOSPHONATE LEAP 4	
1029	1lhb	B	54	353	1.7e-34			51.71	INTERLEUKIN-1 BETA; CHAIN: A; TYPE 1 INTERLEUKIN-1 RECEPTOR; CHAIN: B;	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
										GLYCOPROTEIN, RECEPTOR, 2 SIGNAL, COMPLEX (IMMUNOGLOBULIN/RECEPTOR)
1029	1kb5	H	133	351	1.7e-08			39.81	KE5-C20 T-CELL ANTIGEN RECEPTOR; CHAIN: A, B; ANTIBODY DESIRE-1; CHAIN: L, H	COMPLEX (IMMUNOGLOBULIN/RECEPTOR)
1029	1mam	H	139	349	1.2e-11			36.22	IMMUNOGLOBULIN ANTIGEN-BINDING FRAGMENT (FAB) (ICG2B, KAPPA) 1MAM.3	
1031	1uby		57	398	5.1e-66	-0.31	0.11		FARNESYL DIPHOSPHATE SYNTHASE; CHAIN: NULL;	TRANSFERASE FPS; TRANSFERASE, ISOPRENE BIOSYNTHESIS, CHOLESTEROL BIOSYNTHESIS
1031	1uby		65	397	5.1e-66			70.74	FARNESYL DIPHOSPHATE SYNTHASE; CHAIN: NULL;	TRANSFERASE FPS; TRANSFERASE, ISOPRENE BIOSYNTHESIS, CHOLESTEROL BIOSYNTHESIS
1032	1dfn	A	132	161	1.1e-12			38.55	DEFENSIN DEFENSIN /HNP3-3 IDFN.3	
1032	1dfn	A	133	161	1.1e-12	-0.35	1.00		DEFENSIN DEFENSIN /HNP3-3 IDFN.3	
1032	1dfn	A	133	161	5.1e-11	-0.35	1.00		DEFENSIN DEFENSIN /HNP3-3 IDFN.3	
1034	1a4y	A	66	224	5.7e-22	-0.15	0.35		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPTOPE MAPPING, LEUCINE-RICH 3 REPEATS
1034	1a9n	A	68	208	3.8e-24	0.44	0.78		U2 RNA HAIRPIN IV; CHAIN: Q;	COMPLEX (NUCLEAR

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									R; U2 A'; CHAIN: A, C; U2 B*'; CHAIN: B, D;	PROTEIN(RNA) COMPLEX (NUCLEAR PROTEIN(RNA), RNA, SNRNP RIBONUCLEOPROTEIN)
1034	1a9n	A	93	249	1.3e-21	0.15	0.57		U2 RNA HAIRPIN IV; CHAIN: Q; R; U2 A'; CHAIN: A, C; U2 B*'; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN(RNA) COMPLEX (NUCLEAR PROTEIN(RNA), RNA, SNRNP RIBONUCLEOPROTEIN)
1034	1a9n	C	68	208	1.1e-23	0.52	0.80		U2 RNA HAIRPIN IV; CHAIN: Q; R; U2 A'; CHAIN: A, C; U2 B*'; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN(RNA) COMPLEX (NUCLEAR PROTEIN(RNA), RNA, SNRNP RIBONUCLEOPROTEIN)
1034	1a9n	C	93	249	9.5e-21	0.21	0.62		U2 RNA HAIRPIN IV; CHAIN: Q; R; U2 A'; CHAIN: A, C; U2 B*'; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN(RNA) COMPLEX (NUCLEAR PROTEIN(RNA), RNA, SNRNP RIBONUCLEOPROTEIN)
1034	1c66	A	279	363	3.8e-06	0.12	0.05		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
1034	1cvs	C	283	364	7.6e-07	0.27	0.22		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1034	1cvs	D	283	367	1.5e-06	0.15	0.25		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1034	1d0b	A	39	186	8.5e-19	0.22	0.74		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1034	1d0b	A	44	223	1.9e-24	0.13	0.58		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1034	1dce	A	106	218	1e-09	-0.25	0.03		RAB GERANYLGERANYLTRANSFERASE R4SE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRANSFERASE BETA SUBUNIT; CHAIN: B, D;	ADHESION TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 Å 2 RESOLUTION, N- FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
1034	1dce	A	38	235	1.9e-16	0.05	-0.01		RAB GERANYLGERANYLTRANSFERASE R4SE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRANSFERASE BETA SUBUNIT; CHAIN: B, D;	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 Å 2 RESOLUTION, N- FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
1034	1ds9	A	104	245	1e-08	-0.75	0.10		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE- RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA
1034	1ds9	A	45	208	7.6e-21	-0.55	0.04		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE- RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA
1034	1epf	A	279	358	5.7e-07	0.10	0.98		NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	CELL ADHESION NCAM: NCAM, IMMUNOGLOBULIN FOLD, GLYCOPROTEIN
1034	1ev2	E	276	373	1.5e-06	0.15	0.33		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGFR2; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I- SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1034	1ev2	G	283	358	3.8e-06	0.12	0.77		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGFR2; FGFR2;

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fst Blast	Verify score	PMF score	SEQFOLD score	Coumpound	PDB annotation
									FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H,	IMMUNOGLOBULIN (G) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1034	1fo1	A	183	230	0.0013	-0.40	0.25		NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP-RBD OR RRM) AND LEUCINE-RICH-REPEAT 2 (LRR)
1034	1fo1	B	183	236	0.00076	-0.61	0.05		NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP-RBD OR RRM) AND LEUCINE-RICH-REPEAT 2 (LRR)
1034	1ut		280	356	5.7e-06	0.21	0.01		TITIN, I27; CHAIN: NULL;	IMMUNOGLOBULIN-LIKE DOMAIN CONNECTIN I27, TITIN IG REPEAT 27; MUSCLE PROTEIN
1034	1um		279	358	1.7e-06	0.23	0.34		MUSCLE PROTEIN TITIN MODULE M5 (CONNECTIN) ITNM3 (NMR, MINIMIZED AVERAGE STRUCTURE) ITNM4 ITNM58	IMMUNOGLOBULIN-LIKE DOMAIN
1034	1ww	X	394	490	1.7e-09	0.25	-0.19		NERVE GROWTH FACTOR; CHAIN: V, W; TRKA RECEPTOR; CHAIN: X, Y;	NERVE GROWTH FACTOR/TRKA COMPLEX BETA-NGF; COMPLEX, TRKA RECEPTOR, NERVE GROWTH FACTOR, CYSTEINE KNOT, 2 IMMUNOGLOBULIN LIKE DOMAIN, NERVE GROWTH FACTOR/TRKA COMPLEX
1034	1yge	A	44	198	7.6e-19	-0.34	0.24		GTPASE-ACTIVATING PROTEIN RNA1_SCHPO; CHAIN: A, B;	TRANSCRIPTION RNAIP; RANGAP; GTPASE-ACTIVATING PROTEIN FOR SP11, GTPASE-ACTIVATING PROTEIN, GAP, RNAIP, RANGAP, LRR, LEUCINE-2 RICH REPEAT PROTEIN, TWINNING,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fsl Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										HEMIHEDRAL TWINNING, 3 MEROHEDRAL TWINNING, MEROHEDRY
1034	3icm	A	279	358	9.5e-07	0.40	0.46		NEURAL CELL ADHESION MOLECULE, LARGE ISOFORM; CHAIN: A;	CELL ADHESION PROTEIN NCAM MODULE 2; CELL ADHESION, GLYCOPROTEIN, HEPARIN-BINDING, GPI-ANCHOR, 2 NEURAL ADHESION MOLECULE, IMMUNOGLOBULIN FOLD, HOMOPHILIC 3 BINDING, CELL ADHESION PROTEIN
1035	1cke	A	360	519	0.0019	-0.10	0.12		CYTIDINE MONOPHOSPHATE KINASE; CHAIN: A;	TRANSFERASE CK, MSSA; NUCLEOTIDE MONOPHOSPHATE KINASE, TRANSFERASE
1035	1coz	A	193	312	1.1e-11	0.18	0.18		GLYCEROL-3-PHOSPHATE CYTIDYLTRANSFERASE; CHAIN: A, B;	TRANSFERASE TRANSFERASE
1035	1d6j	A	359	393	1.9e-05	-0.55	0.35		ADENOSINE-5'PHOSPHOSULFATE KINASE; CHAIN: A, B;	TRANSFERASE APS KINASE; APS KINASE, ADENYLYLSULFATE KINASE, SULFATE, NUCLEOTIDE 2 KINASE, TRANSFERASE
1038	1eth	A	1	319	0			112.24	TRIACYLGLYCEROL ACYL-HYDROLASE; CHAIN: A, C; COLIPASE; CHAIN: B, D	COMPLEX (HYDROLASE/COFACTOR) TRIACYLGLYCEROL LIPASE; COMPLEX (HYDROLASE/COFACTOR), LIPID DEGRADATION
1038	1gpl		2	316	0			107.65	R22 LIPASE; CHAIN: NULL;	SERINE ESTERASE RELATED PROTEIN 2 LIPASE; SERINE ESTERASE, HYDROLASE, LIPID DEGRADATION, PANCREAS, 2 GLYCOPROTEIN, CHIMERIC

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fst Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1038	lip1	A	1	318	0			107.77	HYDROLASE(CARBOXYLIC ESTERASE) LIPASE (E.C.3.1.1.3) (TRIACYLGLYCEROL HYDROLASE) ILPB 3	
1038	lipb	B	1	316	0			109.40	HYDROLASE(CARBOXYLIC ESTERASE) LIPASE (E.C.3.1.1.3) COMPLEXED WITH COLIPASE AND INHIBITED ILPB 3 BY UNDECANE PHOSPHONATE METHYL ESTER (TWO CONFORMATIONS) ILPB 4	
1038	lrp1		2	316	0			100.01	PANCREATIC LIPASE RELATED PROTEIN 1; CHAIN: NULL;	HYDROLASE HYDROLASE, LIPID DEGRADATION, PANCREATIC LIPASE
1044	lahd	P	154	219	3.4e-34	0.19	1.00		DNA-BINDING PROTEIN ANTENNAPEDIA PROTEIN (HOMEODOMAIN) MUTANT WITH CYS 39 LAHD 3 REPLACED BY SER (C39S) COMPLEX WITH DNA (NMR, LAHD 4 16 STRUCTURES) LAHD 5	
1044	lan7	A	145	213	3.8e-26	-0.39	0.65		PII-1; CHAIN: A, B; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) GHF-1; COMPLEX (DNA-BINDING PROTEIN/DNA) PITUITARY, CPHD, 2 POU DOMAIN, TRANSCRIPTION FACTOR
1044	lbt2	A	158	215	1.7e-27	0.20	1.00		HOMEODOMAIN PROTEIN HOX-B1; CHAIN: A; PBX1; CHAIN: B; DNA CHAIN: D; DNA CHAIN: E; ULTRABITHORAX HOMEOTIC PROTEIN IV; CHAIN: A;	PROTEIN/DNA HOMEODOMAIN, DNA, COMPLEX, DNA-BINDING PROTEIN, PROTEIN/DNA
1044	lbt8	A	158	212	5.1e-29	0.33	1.00		HOMEODOMAIN PROTEIN	TRANSCRIPTION/DNA ULTRABITHORAX; PBX PROTEIN; DNA BINDING, HOMEODOMAIN,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fst Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									ANTENNAPEDIA PROTEIN (HOMODOMAIN) MUTANT WITH CYS 39 ISAN 3 REPLACED BY SER AND RESIDUES 1-6 DELETED (C39S, DEL 1-6) ISAN 4 (NMR, 20 STRUCTURES) ISAN 5	
1046	1a4y	A	41	214	0.0095	0.27	0.46		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPTIOTYPE MAPPING, LEUCINE-RICH 3 REPEATS
1048	1c1e	A	6	187	6.8e-22	-0.08	0.40		CYTIDINE MONOPHOSPHATE KINASE; CHAIN: A;	TRANSFERASE CK, MSSA; NUCLEOTIDE MONOPHOSPHATE KINASE, TRANSFERASE
1048	1a6j	A	3	187	3.4e-23	0.08	0.33		ADENOSINE-3'PHOSPHOSULFATE KINASE; CHAIN: A, B;	TRANSFERASE APS KINASE, APS KINASE, ADENYL SULFATE KINASE, SULFATE, NUCLEOTIDE 2 KINASE, TRANSFERASE
1048	1q19	A	3	185	1.7e-21	0.34	0.99		URIDYL MONOPHOSPHATE/CYTIDYL MONOPHOSPHATE KINASE; CHAIN: A;	KINASE UNP/CMF KINASE; NUCLEOSIDE MONOPHOSPHATE KINASE, NMP KINASE, PHOSPHORYL 2 TRANSFER, TRANSITION STATE ANALOG COMPLEX, TRANSFERASE
1048	1shk	A	1	186	1.7e-20	-0.06	0.84		SHIKIMATE KINASE; CHAIN: A, B;	TRANSFERASE SHIKIMATE KINASE, PHOSPHORYL TRANSFER, ADP, SHIKIMATE 2 PATHWAY, P-LOOP PROTEIN, TRANSFERASE
1048	1ukz		6	185	1.4e-19	0.35	0.64		TRANSFERASE URIDYLATE KINASE (EC 2.7.4.-)	

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	F ₅₀ Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1048	2cmk	A	6	187	1.7e-21	0.01	0.12		COMPLEXED WITH ADP AND AMP 1UKZ 3	TRANSFERASE CK; NUCLEOTIDE MONOPHOSPHATE KINASE, CHAIN: A;
1048	3adk		3	184	8.5e-22	-0.02	0.22		TRANSFERASE(PHOSPHOTRANSFERASE) ADENYLATE KINASE (E.C.2.7.4.3) 3ADK 4	
1049	1axi	B	162	349	1.7e-10	0.18	0.48		GROWTH HORMONE; CHAIN: A; GROWTH HORMONE RECEPTOR; CHAIN: B; HEMOLIN; CHAIN: A, B;	COMPLEX (HORMONE/RECEPTOR) HGH; HGHBP; COMPLEX (HORMONE/RECEPTOR)
1049	1b1h	A	2	338	6.8e-21	0.21	-0.14			INSECT IMMUNITY INSECT IMMUNITY 1PS-BINDING, HOMOPHILIC ADHESION
1049	1b1j8		253	350	1.9e-14	0.35	0.42		GP130; CHAIN: NULL;	RECEPTOR RECEPTOR, SIGNAL TRANSDUCER OF IL-6 TYPE CYTOKINES, THIRD 2 N-TERMINAL DOMAIN, TRANSMEMBRANE, GLYCOPROTEIN
1049	1b1j8		360	461	3.8e-09	0.07	0.33		GP130; CHAIN: NULL;	RECEPTOR RECEPTOR, SIGNAL TRANSDUCER OF IL-6 TYPE CYTOKINES, THIRD 2 N-TERMINAL DOMAIN, TRANSMEMBRANE, GLYCOPROTEIN
1049	1b1j8		477	568	8.5e-12	0.27	0.01		GP130; CHAIN: NULL;	RECEPTOR RECEPTOR, SIGNAL TRANSDUCER OF IL-6 TYPE CYTOKINES, THIRD 2 N-TERMINAL DOMAIN, TRANSMEMBRANE, GLYCOPROTEIN
1049	1b1j8		573	674	5.7e-19	0.25	0.35		GP130; CHAIN: NULL;	RECEPTOR RECEPTOR, SIGNAL TRANSDUCER OF IL-6 TYPE CYTOKINES, THIRD 2 N-TERMINAL DOMAIN, TRANSMEMBRANE,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
1049	1bqu	A	358	581	1.7e-14	-0.05	0.10		GP130; CHAIN: A, B;	SIGNALING PROTEIN CYTOKINE RECEPTOR, GLYCOPROTEIN 130, GP130, INTERLEUKINE 6 2 RECEPTOR BETA SUBUNIT, SIGNALING PROTEIN
1049	1bqu	A	479	681	6.8e-23	0.04	0.09		GP130; CHAIN: A, B;	SIGNALING PROTEIN CYTOKINE RECEPTOR, GLYCOPROTEIN 130, GP130, INTERLEUKINE 6 2 RECEPTOR BETA SUBUNIT, SIGNALING PROTEIN
1049	1c8p	A	256	352	3.8e-13	0.36	0.35		CYTOKINE RECEPTOR COMMON BETA CHAIN; CHAIN: A;	MEMBRANE PROTEIN BETA SANDWICH, CYTOKINE RECEPTOR, FN3 DOMAIN
1049	1c8p	A	359	437	7.6e-09	0.28	-0.12		CYTOKINE RECEPTOR COMMON BETA CHAIN; CHAIN: A;	MEMBRANE PROTEIN BETA SANDWICH, CYTOKINE RECEPTOR, FN3 DOMAIN
1049	1cd9	B	159	356	9.5e-27	0.17	0.24		GRANULOCYTE COLONY-STIMULATING FACTOR; CHAIN: A, C; G-CSF RECEPTOR; CHAIN: B, D;	CYTOKINE G-CSF; G-CSF-R, CLASS I CYTOKINE, HEMATOPOIETIC RECEPTOR, SIGNAL TRANSDUCTION
1049	1cd9	B	360	564	7.6e-16	0.14	0.06		GRANULOCYTE COLONY-STIMULATING FACTOR; CHAIN: A, C; G-CSF RECEPTOR; CHAIN: B, D;	CYTOKINE G-CSF; G-CSF-R, CLASS I CYTOKINE, HEMATOPOIETIC RECEPTOR, SIGNAL TRANSDUCTION
1049	1cfb		156	350	1.1e-34	-0.07	0.55		NEURAL ADHESION MOLECULE DROSOPHILA NEUROGLIAN (CITOMOTRYPTIC FRAGMENT CONTAINING THE ICFB 3 TWO AMINO PROXIMAL FIBRONECTIN TYPE III REPEATS 1CFB 4 (RESIDUES 610 - 814)) ICFB 5	NEURAL ADHESION
1049	1cfb		255	456	1.9e-23	0.20	0.90		NEURAL ADHESION	

SEQ NO:	PDB ID	CITAI N ID	STAR T AA	END AA	Fsi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									MOLECULE DROSOPHILA NEUROGLIAN (CHYMOTRYPTIC FRAGMENT CONTAINING THE ICFB 3 TWO AMINO PROXIMAL FIBRONECTIN TYPE III REPEATS ICFB 4 (RESIDUES 610 - 814)) ICFB 5	
1049	1c1b		475	675	3.8e-31	0.17	0.42		NEURAL ADHESION MOLECULE DROSOPHILA NEUROGLIAN (CHYMOTRYPTIC FRAGMENT CONTAINING THE ICFB 3 TWO AMINO PROXIMAL FIBRONECTIN TYPE III REPEATS ICFB 4 (RESIDUES 610 - 814)) ICFB 5	
1049	1c1b		479	670	1e-18	0.35	0.06		NEURAL ADHESION MOLECULE DROSOPHILA NEUROGLIAN (CHYMOTRYPTIC FRAGMENT CONTAINING THE ICFB 3 TWO AMINO PROXIMAL FIBRONECTIN TYPE III REPEATS ICFB 4 (RESIDUES 610 - 814)) ICFB 5	
1049	1cs6	A	272	671	6.8e-23	0.00	-0.20		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
1049	1cs6	A	2	349	1.7e-35	0.15	-0.08		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
1049	1cs6	A	350	750	3.4e-15	0.12	-0.17		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
1049	1cs6	A	67	464	6.8e-30	-0.08	0.10		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION

SEQ NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQOL D score	Compound	PDB annotation
1049	1cto		157	247	7.6e-13	-0.16	0.04		GRANULOCYTE COLONY-STIMULATING FACTOR RECEPTOR; CHAIN: NULL;	BINDING PROTEIN BINDING PROTEIN, CYTOKINE RECEPTOR
1049	1cto		259	350	3.8e-13	0.12	0.09		GRANULOCYTE COLONY-STIMULATING FACTOR RECEPTOR; CHAIN: NULL;	BINDING PROTEIN BINDING PROTEIN, CYTOKINE RECEPTOR
1049	1cto		479	585	7.6e-10	0.47	-0.09		GRANULOCYTE COLONY-STIMULATING FACTOR RECEPTOR; CHAIN: NULL;	BINDING PROTEIN BINDING PROTEIN, CYTOKINE RECEPTOR
1049	1cws	C	74	250	6.8e-31	0.25	0.42		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1049	1cws	D	2	135	1.5e-15	0.02	-0.15		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1049	1cws	D	61	153	5.7e-20	-0.01	0.19		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1049	1cws	D	74	250	1.7e-28	-0.03	0.51		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1049	1ccr	B	474	555	1.5e-07	0.08	0.13		ERYTHROPOIETIN; CHAIN: A;	COMPLEX (CYTOKINE/RECEPTOR)

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fst Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									ERYTHROPOIETIN RECEPTOR; CHAIN: B, C;	EPORP; ERYTHROPOIETIN, ERYTHROPOIETIN RECEPTOR, SIGNAL 2 TRANSDUCTION, HEMATOPOIETIC CYTOKINE, CYTOKINE RECEPTOR 3 CLASS 1, COMPLEX (CYTOKINE/RECEPTOR)
1049	1epf	A	67	222	3.8e-14	0.02	0.27		NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	CELL ADHESION NCAM; NCAM, IMMUNOGLOBULIN FOLD, GLYCOPROTEIN
1049	1epf	A	71	234	6.8e-13	0.13	0.07		NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	CELL ADHESION NCAM; NCAM, IMMUNOGLOBULIN FOLD, GLYCOPROTEIN
1049	1ev2	E	74	230	1.7e-26	-0.02	0.65		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGFR2; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1049	1ev2	G	74	234	3.4e-30	-0.14	0.12	-	FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGFR2; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1049	1evt	C	64	213	5.7e-20	-0.08	0.58		FIBROBLAST GROWTH FACTOR 1; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGFR1; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1049	1evt	C	74	230	1.7e-26	0.05	0.63		FIBROBLAST GROWTH FACTOR 1; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGFR1; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Fsi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1049	1f6f	B	160	354	3.4e-24	0.28	0.51		C, D;	SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
									PLACENTAL LACTOGEN; CHAIN: A; PROLACTIN RECEPTOR; CHAIN: B, C;	HORMONE/GROWTH FACTOR/HORMONE RECEPTOR 4- HELICAL BUNDLE, ALPHA HELICAL BUNDLE, TERNARY COMPLEX, FN 2 III DOMAINS, BETA SHEET DOMAINS, CYTOKINE-RECEPTOR COMPLEX
1049	1f6f	B	70	253	1.7e-16	-0.23	0.03		PLACENTAL LACTOGEN; CHAIN: A; PROLACTIN RECEPTOR; CHAIN: B, C;	HORMONE/GROWTH FACTOR/HORMONE RECEPTOR 4- HELICAL BUNDLE, ALPHA HELICAL BUNDLE, TERNARY COMPLEX, FN 2 III DOMAINS, BETA SHEET DOMAINS, CYTOKINE-RECEPTOR COMPLEX
1049	1f6f	C	192	352	7.6e-10	-0.11	0.71		PLACENTAL LACTOGEN; CHAIN: A; PROLACTIN RECEPTOR; CHAIN: B, C;	HORMONE/GROWTH FACTOR/HORMONE RECEPTOR 4- HELICAL BUNDLE, ALPHA HELICAL BUNDLE, TERNARY COMPLEX, FN 2 III DOMAINS, BETA SHEET DOMAINS, CYTOKINE-RECEPTOR COMPLEX
	1fng	A	475	572	5.1e-08	0.18	-0.20		TELOKIN; CHAIN: A	CONTRACTILE PROTEIN IMMUNOGLOBULIN FOLD, BETA BARREL
1049	1fna		486	565	1.7e-13	0.23	0.16		CELL ADHESION PROTEIN FIBRONECTIN CELL-ADHESION MODULE TYPE III-10, IFNA 3	
1049	1fna		779	866	6.8e-09	0.38	-0.20		CELL ADHESION PROTEIN FIBRONECTIN CELL-ADHESION MODULE TYPE III-10, IFNA 3	

SEQ ID NO:	PDB ID	CLAI ID	STAR T AA	END AA	Fsi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1049	1mf		158	565	5.1e-36	0.25	0.98		FIBRONECTIN; 1NF 6 CHAIN; NULL; 1NF 7	CELL ADHESION PROTEIN RGD, EXTRACELLULAR MATRIX IFNF 18
1049	1mf		159	575	5.1e-36			166.16	FIBRONECTIN; 1NF 6 CHAIN; NULL; 1NF 7	CELL ADHESION PROTEIN RGD, EXTRACELLULAR MATRIX IFNF 18
1049	1mf		479	866	3.4e-33	0.29	0.23		FIBRONECTIN; 1NF 6 CHAIN; NULL; 1NF 7	CELL ADHESION PROTEIN RGD, EXTRACELLULAR MATRIX IFNF 18
1049	1mf		68	439	1.7e-26	0.24	0.76		FIBRONECTIN; 1NF 6 CHAIN; NULL; 1NF 7	CELL ADHESION PROTEIN RGD, EXTRACELLULAR MATRIX IFNF 18
1049	1mf		772	977	3.4e-12	0.08	-0.20		FIBRONECTIN; 1NF 6 CHAIN; NULL; 1NF 7	CELL ADHESION PROTEIN RGD, EXTRACELLULAR MATRIX IFNF 18
1049	1fh	A	272	564	1.7e-20	0.22	0.55		FIBRONECTIN; CHAIN: A;	HEPARIN AND INTEGRIN BINDING
1049	1fh	A	361	664	3.4e-27	0.26	0.07		FIBRONECTIN; CHAIN: A;	HEPARIN AND INTEGRIN BINDING
1049	1fh	A	482	751	3.4e-23	0.12	-0.07		FIBRONECTIN; CHAIN: A;	HEPARIN AND INTEGRIN BINDING
1049	1fh	A	580	855	8.5e-25	0.01	-0.19		FIBRONECTIN; CHAIN: A;	HEPARIN AND INTEGRIN BINDING
1049	1fh	A	70	333	1.4e-18	0.29	0.98		FIBRONECTIN; CHAIN: A;	HEPARIN AND INTEGRIN BINDING
1049	1fh	A	774	977	3.4e-20	0.05	-0.20		FIBRONECTIN; CHAIN: A;	HEPARIN AND INTEGRIN BINDING
1049	1mf		137	343	1.1e-27	0.21	1.00		FIBRONECTIN; CHAIN: NULL;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN RGD, EXTRACELLULAR MATRIX, 2
									GLYCOPROTEIN, HEPARIN-BINDING,	
1049	1mf		162	343	3.4e-14	0.03	1.00		FIBRONECTIN; CHAIN: NULL;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN RGD, EXTRACELLULAR MATRIX, 2
										HEPARIN-BINDING, GLYCOPROTEIN
1049	1mf		259	456	1.1e-20	-0.04	0.49		FIBRONECTIN; CHAIN: NULL;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN RGD,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T.AA	END AA	Fsi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1049	1mfn	272	459	6.8e-11	0.13	0.45			FIBRONECTIN; CHAIN: NULL;	EXTRACELLULAR MATRIX, 2 HEPARIN-BINDING, GLYCOPROTEIN
1049	1mfn	360	565	3.4e-20	0.05	0.13			FIBRONECTIN; CHAIN: NULL;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN, RGD, EXTRACELLULAR MATRIX, 2 HEPARIN-BINDING, GLYCOPROTEIN
1049	1mfn	482	665	1.9e-27	0.24	0.17			FIBRONECTIN; CHAIN: NULL;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN, RGD, EXTRACELLULAR MATRIX, 2 HEPARIN-BINDING, GLYCOPROTEIN
1049	1mfn	482	665	6.8e-25	0.20	-0.05			FIBRONECTIN; CHAIN: NULL;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN, RGD, EXTRACELLULAR MATRIX, 2 HEPARIN-BINDING, GLYCOPROTEIN
1049	1net	64	152	9.5e-23	0.16	1.00			TTTN; CHAIN: NULL;	MUSCLE PROTEIN CONNECTIN, NEXTM5; CELL ADHESION, GLYCOPROTEIN
1049	1gg3	A	160	352	1.2e-15	0.19	0.99		INTEGRIN BETA-4 SUBUNIT; CHAIN: A, B;	TRANSMEMBRANE, REPEAT, BRAIN; 2 IMMUNOGLOBULIN FOLD, ALTERNATIVE SPLICING, SIGNAL, 3 MUSCLE PROTEIN
1049	1gg3	A	160	352	1.2e-15	0.19	0.99		INTEGRIN BETA-4 SUBUNIT; CHAIN: A, B;	STRUCTURAL PROTEIN INTEGRIN, HEMIDESMOSOME, FIBRONECTIN, CARCINOMA, STRUCTURAL 2 PROTEIN

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fs1 Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1049	1qg3	A	361	569	3.4e-19	0.11	0.59		INTEGRIN BETA-4 SUBUNIT; CHAIN: A, B;	STRUCTURAL PROTEIN INTEGRIN, HEMIDESMOSOME, FIBRONECTIN, CARCINOMA, STRUCTURAL 2
1049	1qg3	A	479	677	5.1e-26			103.51	INTEGRIN BETA-4 SUBUNIT; CHAIN: A, B;	STRUCTURAL PROTEIN INTEGRIN, HEMIDESMOSOME, FIBRONECTIN, CARCINOMA, STRUCTURAL 2
1049	1qg3	A	481	663	5.1e-26	0.23	0.43		INTEGRIN BETA-4 SUBUNIT; CHAIN: A, B;	STRUCTURAL PROTEIN INTEGRIN, HEMIDESMOSOME, FIBRONECTIN, CARCINOMA, STRUCTURAL 2
1049	1qg3	A	68	248	3.4e-17	0.29	0.66		INTEGRIN BETA-4 SUBUNIT; CHAIN: A, B;	STRUCTURAL PROTEIN INTEGRIN, HEMIDESMOSOME, FIBRONECTIN, CARCINOMA, STRUCTURAL 2
1049	1qr4	A	360	564	6.8e-12	0.24	0.43		TENASCIN; CHAIN: A, B;	STRUCTURAL PROTEIN TENASCIN, FIBRONECTIN TYPE-III, HEPARIN, EXTRACELLULAR 2 MATRIX, ADHESION, FUSION PROTEIN, STRUCTURAL PROTEIN
1049	1qr4	A	711	862	3.4e-08	0.09	-0.20		TENASCIN; CHAIN: A, B;	STRUCTURAL PROTEIN TENASCIN, FIBRONECTIN TYPE-III, HEPARIN, EXTRACELLULAR 2 MATRIX, ADHESION, FUSION PROTEIN, STRUCTURAL PROTEIN
1049	1qr4	A	776	971	3.4e-11	0.08	-0.20		TENASCIN; CHAIN: A, B;	STRUCTURAL PROTEIN TENASCIN, FIBRONECTIN TYPE-III, HEPARIN, EXTRACELLULAR 2 MATRIX, ADHESION, FUSION PROTEIN, STRUCTURAL PROTEIN
1049	1tit		65	150	1.1e-19	0.70	0.15		TITIN, I27; CHAIN: NULL;	IMMUNOGLOBULIN-LIKE DOMAIN CONNECTIN I27, TITIN IG REPEAT 27, MUSCLE PROTEIN,

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1049	1tmn		67	152	1.9e-22	0.39	0.84		MUSCLE PROTEIN TITIN MODULE M5 (CONNECTIN) ITNM 3 (NMR, MINIMIZED AVERAGE STRUCTURE) ITNM 4 ITNM 58	IMMUNOGLOBULIN-LIKE DOMAIN
1049	1ttf		776	866	1.7e-09	0.39	-0.20		GLYCOPROTEIN FIBRONECTIN (TENTH TYPE III MODULE) (NMR, 36 STRUCTURES) ITTF 3	
1049	1wtl		65	152	1.9e-22	0.66	-0.09		TWITCHIN 18TH IGSF MODULE; CHAIN: NULL;	MUSCLE PROTEIN IMMUNOGLOBULIN SUPERFAMILY, I SET, MUSCLE PROTEIN
1049	1wvc	A	64	163	1.1e-21	0.18	0.59		NT-3 GROWTH FACTOR RECEPTOR TRKC; CHAIN: A;	TRANSFERASE TRK RECEPTOR RECEPTOR TYROSINE KINASE, 3D-DOMAIN SWAPPING, 2
1049	2fcb	A	60	251	9.5e-13	-0.00	0.01		FC GAMMA RIIB; CHAIN: A;	IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32, IMMUNE SYSTEM
1049	2fcb	A	154	250	1.5e-14	0.55	0.68		FIBRONECTIN; CHAIN: A;	PROTEIN BINDING ED-B, FIBRONECTIN, TYPEII DOMAIN, ANGIOGENESIS, PROTEIN 2
1049	2fcb	A	255	345	9.5e-14	0.76	0.16		FIBRONECTIN; CHAIN: A;	PROTEIN BINDING ED-B, FIBRONECTIN, TYPEII DOMAIN, ANGIOGENESIS, PROTEIN 2
1049	2fcb	A	359	465	9.5e-10	0.02	0.10		FIBRONECTIN; CHAIN: A;	PROTEIN BINDING ED-B, FIBRONECTIN, TYPEII DOMAIN, ANGIOGENESIS, PROTEIN 2
1049	2fcb	A	475	570	1.9e-13	-0.12	0.04		FIBRONECTIN; CHAIN: A;	PROTEIN BINDING ED-B, FIBRONECTIN, TYPEII DOMAIN, ANGIOGENESIS, PROTEIN 2

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fsi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1049	2fns	A	574	670	1.5e-16	0.10	0.28		FIBRONECTIN; CHAIN: A;	PROTEIN BINDING ED-B, FIBRONECTIN, TYPEIII DOMAIN, ANGIOGENESIS, PROTEIN 2 BINDING
1049	3hrh	B	162	349	1e-10	0.16	0.13		HORMONE/RECEPTOR HUMAN GROWTH HORMONE COMPLEXED WITH ITS RECEPTOR 3HHR 3 (EXTRACELLULAR DOMAIN) 3HHR 4	
1049	3hrh	B	162	351	3.8e-27	0.24	0.03		HORMONE/RECEPTOR HUMAN GROWTH HORMONE COMPLEXED WITH ITS RECEPTOR 3HHR 3 (EXTRACELLULAR DOMAIN) 3HHR 4	
1049	3ncm	A	65	154	3.8e-23	0.45	0.46		NEURAL CELL ADHESION MOLECULE, LARGE ISOFORM; CHAIN: A;	CELL ADHESION PROTEIN NCAM MODULE 2; CELL ADHESION, GLYCOPROTEIN, HEPARIN-BINDING, GPI-ANCHOR, 2 NEURAL ADHESION MOLECULE, IMMUNOGLOBULIN FOLD, HOMOPHILIC 3 BINDING, CELL ADHESION PROTEIN
1050	1blh	A	20	157	3.4e-29	0.09	-0.06		HEMOLIN; CHAIN: A, B;	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION
1050	1es6	A	4	158	3.4e-34	0.02	0.07		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
1050	1evs	C	3	157	3.4e-41	0.12	-0.05		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN:	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fsi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1050	1ews	D	3	157	6.8e-42	0.22	0.33		C, D; FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1050	1epf	A	2	143	6.8e-22	-0.00	0.64		NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	CELL ADHESION NCAM, IMMUNOGLOBULIN FOLD, GLYCOPROTEIN
1050	1ev2	E	3	157	1.7e-36	0.08	0.05		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGFR2, FGFR2; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE L-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1050	1ev2	E	90	162	8.5e-14	0.21	-0.05		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2, FGFR2; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE L-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1050	1evt	C	3	157	1e-41	0.08	0.54		FIBROBLAST GROWTH FACTOR 1; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF1, FGFR1; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE L-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1050	1l2q	A	2	162	1.7e-23	0.19	0.54		HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A;	IMMUNE SYSTEM FC-EPSILON RI-ALPHA; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, JGE-BINDING 2 PROTEIN
1050	1f6g	A	2	159	8.5e-24	-0.02	0.90		FC RECEPTOR	IMMUNE SYSTEM, MEMBRANE

SEQ NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fsi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									FC(GAMMA)RIIA; CHAIN: A;	PROTEIN CD32; FC RECEPTOR, IMMUNOGLOBULIN, LEUKOCYTE, CD32
1050	1fug	A	1	75	1.2e-12	-0.10	0.63		TELOKIN; CHAIN: A	CONTRACTILE PROTEIN IMMUNOGLOBULIN FOLD, BETA A BARREL
1050	1fug	A	76	157	3.4e-17	0.37	-0.14		TELOKIN; CHAIN: A	CONTRACTILE PROTEIN IMMUNOGLOBULIN FOLD, BETA BARREL
1050	1fnl	A	2	147	1.9e-20	0.00	0.31		LOW AFFINITY IMMUNOGLOBULIN GAMMA FC REGION CHAIN: A;	IMMUNE SYSTEM RECEPTOR BETA SANDWICH, IMMUNOGLOBULIN-LIKE RECEPTOR
1050	1nct		2	75	1.2e-12	0.07	0.87		TITIN; CHAIN: NULL;	MUSCLE PROTEIN CONNECTIN, NEXTM5: CELL ADHESION, GLYCOPROTEIN, TRANSMEMBRANE, REPEAT, BRAIN, 2 IMMUNOGLOBULIN FOLD, ALTERNATIVE SPLICING, SIGNAL, 3
1050	1nct		80	158	1.7e-16	0.20	-0.09		TITIN; CHAIN: NULL;	MUSCLE PROTEIN CONNECTIN, NEXTM5: CELL ADHESION, GLYCOPROTEIN, TRANSMEMBRANE, REPEAT, BRAIN, 2 IMMUNOGLOBULIN FOLD, ALTERNATIVE SPLICING, SIGNAL, 3
1050	1tnm		2	75	1.2e-12	0.43	0.54		MUSCLE PROTEIN TITIN MODULE M5 (CONNECTIN) 1TNM 3 (NMR, MINIMIZED AVERAGE STRUCTURE) 1TNM 4 1TNM 58	MUSCLE PROTEIN
1050	1tnm		80	158	1.7e-16	0.07	-0.12		MUSCLE PROTEIN TITIN MODULE M5 (CONNECTIN) 1TNM 3 (NMR, MINIMIZED	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fsi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									AVERAGE STRUCTURE) ITNM 4 ITNM 58	
1050	2dli	A	2	146	1.9e-19	-0.26	0.09		MHC CLASS I NK CELL RECEPTOR PRECURSOR; CHAIN: A;	IMMUNE SYSTEM P58 NATURAL KILLER CELL RECEPTOR, KIR, NATURAL KILLER RECEPTOR, INHIBITORY RECEPTOR, 2 IMMUNOGLOBULIN
1050	25cb	A	2	160	6.8e-25	0.14	0.69		FC GAMMA RIIB; CHAIN: A;	IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32, IMMUNE SYSTEM
1051	1aln	A	26	115	3.4e-43	-0.16	0.30		B*3501; CHAIN: A, B; PEPTIDE VPLRMTY; CHAIN: C;	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B*3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)
1051	1agd	A	26	115	3.4e-43	0.06	0.25		B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKKKKYKL - INDEX PEPTIDE); CHAIN: C;	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX
1051	1daz	A	26	115	1.7e-42	0.18	0.22		HLA-A*0201; CHAIN: A, D; BETA-2 MICROGLOBULIN; CHAIN: B, E; HTLV-1 OCTAMERIC TAX PEPTIDE; CHAIN: C, F;	IMMUNE SYSTEM IMMUNOGLOBULIN FOLD
1051	1efx	A	26	115	5.1e-43	0.24	0.28		HLA-CW3 (HEAVY CHAIN); CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; PEPTIDE FROM IMPORTIN ALPHA-2; CHAIN: C; NATURAL KILLER CELL RECEPTOR KIR2DL2; CHAIN: D, E;	IMMUNE SYSTEM MHC, HLA, CLASS I, KIR, NK CELL RECEPTOR, IMMUNOGLOBULIN 2 FOLD, RECEPTOR/MHC COMPLEX
1051	1hoc	A	26	116	1.4e-42	0.34	0.69		HISTOCOMPATIBILITY ANTIGEN MURINE CLASS I	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									MAJOR HISTOCOMPATIBILITY COMPLEX CONSISTING IHOC 3 OF H-2D-B*0801, B2-MICROGLOBULIN, AND A 9-RESIDUE PEPTIDE IHOC 4	
1051	1asb	A	26	115	8.5e-44	0.08	0.40		HISTOCOMPATIBILITY ANTIGEN CLASS I ANTIGEN AW66.1 (LEUCOCYTE IHSB 3 ANTIGEN) IHSB 4	
1051	1mie	A	26	115	8.5e-43	0.13	0.25		HLA CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-E; CHAIN: A; C; BETA-2-MICROGLOBULIN; CHAIN: B; D; PEPTIDE (VMAPTVLL); CHAIN: P; Q;	MAJOR HISTOCOMPATIBILITY COMPLEX MHC NONCLASSICAL CHAIN, MHC-E, HLA-E, MHC CLASS HLA-E, HLA E, MAJOR HISTOCOMPATIBILITY COMPLEX, MHC, ILA, 2 BETA 2 MICROGLOBULIN, PEPTIDE, LEADER PEPTIDE, 3 NON-CLASSICAL MHC, CLASS IB MHC COMPLEX (MHC IPEPTIDE) VSV-8; MHC/PEPTIDE COMPLEX, TRANSMEMBRANE PROTEIN, THYMIC 2 SELECTION, COMPLEX (MHC IPEPTIDE)
1051	1osz	A	26	115	1.2e-43	0.13	0.37		MHC CLASS I H-2KB HEAVY CHAIN; CHAIN: A; BETA-2-MICROGLOBULIN; CHAIN: B; VESICULAR STOMATITIS VIRUS NUCLEOPROTEIN; CHAIN: C;	
1051	1q03	A	26	115	3.4e-42	0.10	0.39		MHC CLASS I H-2DD HEAVY CHAIN; CHAIN: A; BETA-2-MICROGLOBULIN; CHAIN: B; HIV ENVELOPE GLYCOPROTEIN 120 PEPTIDE; CHAIN: P; 1Y49A; CHAIN: C; D;	COMPLEX (NK RECEPTOR) MHC CLASS I H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, B2M; NK-CELL SURFACE GLYCOPROTEIN YEL48, NK CELL, INHIBITORY RECEPTOR, MHC-I, C-TYPE LECTIN-LIKE, 2 HISTOCOMPATIBILITY, B2M, LY49,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1051	1lmc	A	26	115	8.5e-44	0.43	0.52		HISTOCOMPATIBILITY ANTIGEN TRUNCATED HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-A*68 ITMC 3 COMPLEXED WITH A DECAMERIC PEPTIDE (EVAPPEYHRK) ITMC 4	LY-49
1068	1lmc	C	568	650	3.4e-49			100.26	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1068	1lff	A	596	762	8.5e-38			108.39	TTT1A; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1068	2gli	A	327	466	3.4e-34			89.55	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1070	1a25	A	160	291	5.1e-37			68.22	PROTEIN KINASE C (BETA); CHAIN: A, B;	CALCIUM-BINDING PROTEIN CALB; CALCIUM-H/PHOSPHOLIPID BINDING PROTEIN, 2 CALCIUM-BINDING PROTEIN
1070	1rsy		154	283	3.4e-44			97.42	CALCIUM/PHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN-1 (FIRST C2)	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									DOMAIN(CALB) IRSY 3	
1075	1got	B	1	322	5.1e-89			116.65	GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETERODIMER 2 SIGNAL TRANSDUCTION
1078	1got	B	3	345	5.1e-81			104.69	GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETERODIMER 2 SIGNAL TRANSDUCTION
1084	1mey	C	330	412	1.4e-48			107.26	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1084	1if6	A	750	913	1e-37			114.17	TTIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1084	2gll	A	302	441	1.4e-33			103.60	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI;

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQOL D score	Compound	PDB annotation
1090	1evh	A	9	122	3.4e-50			82.80	MENA EVH1 DOMAIN; CHAIN: A; PEPTIDE ACTA; CHAIN: B;	GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1090	1qc6	A	9	121	1.7e-44			62.71	EVH1 DOMAIN FROM ENA/VASP-LIKE PROTEIN; CHAIN: A, B; PHE-GLU-PHE-PRO-PRO-PRO-THR-ASP-GLU-GLU; CHAIN: C, D;	CONTRACTILE PROTEIN WHI DOMAIN; MOLECULAR RECOGNITION, ACTIN DYNAMICS, CONTRACTILE PROTEIN CELL MOTILITY AN INCOMPLETE SEVEN STRANDED ANTI-PARALLEL BETA BARREL 2 CLOSED BY AN ALPHA HELIX, EVH1 DOMAIN, ACTIN-BASED CELL 3 MOTILITY, INTERACTION MODULE
1095	1alh	A	391	473	1.7e-26			84.85	QGRS ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1095	1mev	C	418	500	1.4e-45			110.38	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1095	1lrf6	A	362	530	3.4e-34			120.65	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1095	1ubd	C	336	444	3.4e-33			98.51	YY1; CHAIN: C; ADENOVIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1095	2gli	A	334	473	6.8e-34			105.76	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1101	1cdh	A	62	266	5.1e-48			122.19	E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
1101	1ncj	A	61	265	6.8e-50			122.52	N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN
1105	1aj4		72	227	8.5e-36			73.76	TROPONIN C; CHAIN: NULL;	MUSCLE PROTEIN CTNC; CARDIAC, MUSCLE PROTEIN, REGULATORY, CALCIUM BINDING
1105	1nut	B	74	249	1.7e-39			92.24	SERINE/THREONINE PHOSPHATASE 2B; CHAIN: A, B;	HYDROLASE, PHOSPHATASE, IMMUNOSUPPRESSION
1105	1bjf	A	65	245	1.7e-49			184.52	NEUROCALCIN DELTA; CHAIN: A, B;	CALCIUM-BINDING CALCIUM-BINDING, MYRISTOYLATION, NEURONAL SPECIFIC GUANYLATE 2 CYCLASE ACTIVATOR
1105	1cdm	A	82	234	1.4e-55			57.84	CALCIUM-BINDING PROTEIN CALMODULIN COMPLEXED WITH CALMODULIN-BINDING DOMAIN OF 1CDM 3 CALMODULIN-DEPENDENT PROTEIN KINASE II 1CDM. 4	
1105	1ccl		82	235	3.4e-60			67.88	CALCIUM-BINDING PROTEIN	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1105	1lka		62	245	3.4e-39			160.57	CALMODULIN (VERTEBRATE) ICIL 3 RECOVERIN; CHAIN: NULL;	CALCIUM-BINDING PROTEIN CALCIUM-MYRISTOYL SWITCH, CALCIUM-BINDING PROTEIN
1105	1rec		68	250	1.7e-34			143.82	CALCIUM-BINDING PROTEIN RECOVERIN (CALCIUM SENSOR IN VISION) IREC 3 TROPONIN C; CHAIN: NULL;	
1105	1tef		70	235	1.5e-39			73.38		CALCIUM-REGULATED MUSCLE CONTRACTION MUSCLE BINDING, TROPONIN, E-F HAND, 2 OPEN CONFORMATION REGULATORY DOMAIN, CALCIUM- REGULATED 3 MUSCLE CONTRACTION
1105	1tnx		67	233	1e-38			69.96	TROPONIN C; ITNX 4 CHAIN: NULL; ITNX 5	CALCIUM-BINDING PROTEIN EF- HAND ITNX 14
1105	1top		63	237	8.5e-40			73.36	CONTRACTILE SYSTEM PROTEIN TROPONIN C ITOP 3	
1105	1rvk	A	79	236	3.4e-59			68.28	CALMODULIN; CHAIN: A; RS20; CHAIN: B;	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALING, 2 COMPLEX/CALCIUM-BINDING PROTEIN/PEPTIDE)
1105	2sep	A	34	205	3.4e-09			53.97	BINDING PROTEIN SARCOPLASMIC CALCIUM- BINDING PROTEIN 2SCP 3	
1114	1am4	D	51	216	6.8e-48			70.86	P50-RHO GAP; CHAIN: A, B, C; CDC42HS; CHAIN: D, E, F;	COMPLEX (GTPASE- ACTIVATING/GTP-BINDING) COMPLEX (GTPASE- ACTIVATING/GTP-BINDING), GTPASE ACTIVATION
1114	1byu	A	45	231	8.5e-52			74.78	GTP-BINDING PROTEIN RAN;	TRANSPORT PROTEIN TC4; GTPASE,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fsi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1114	lbya	B	41	231	1.7e-52			69.65	CHAIN: A, B; GTP-BINDING PROTEIN RAN; CHAIN: A, B;	NUCLEAR TRANSPORT, TRANSPORT PROTEIN, TRANSPORT PROTEIN TC4; GTPASE, NUCLEAR TRANSPORT, TRANSPORT PROTEIN
1114	lcly	A	50	216	1.7e-63			67.97	RAS-RELATED PROTEIN RAP-1A; CHAIN: A; PROTO-ONCOGENE SERINE/THREONINE PROTEIN KINASE CHAIN: B;	SIGNALING PROTEIN GTP-BINDING PROTEINS, PROTEIN-PROTEIN COMPLEX, EFFECTORS
1114	lctq	A	50	217	1.7e-62			75.99	TRANSFORMING PROTEIN P21/H-RAS-1; CHAIN: A;	SIGNALING PROTEIN G PROTEIN, GTP HYDROLYSIS, KINETIC CRYSTALLOGRAPHY, 2 SIGNALING PROTEIN
1114	lczx	A	47	222	1.5e-54			82.44	HIS-TAGGED TRANSFORMING PROTEIN RHOA(0-181); CHAIN: A; PKS; CHAIN: B;	SIGNALING PROTEIN PROTEIN-PROTEIN COMPLEX, ANTIPARALLEL COILED-COIL
1114	lhnr	A	37	218	5.1e-12			71.40	HUMAN ADP-RIBOSYLATION FACTOR 1; IHUR 3 CHAIN: A; B; IHUR 7	PROTEIN TRANSPORT GDP-BINDING, MEMBRANE TRAFFICKING, NON-MYRISTOYLATED IHUR 16
1114	libr	A	52	221	3.4e-51			86.05	RAN; CHAIN: A; C; IMPORTIN BETA SUBUNIT; CHAIN: B, D;	SMALL GTPASE KARYOPHERIN BETA, p95 SMALL GTPASE, NUCLEAR TRANSPORT RECEPTOR
1114	lkao		50	217	3.4e-60			79.99	RAP2A; CHAIN: NULL;	GTP-BINDING PROTEIN GTP-BINDING PROTEIN, SMALL GTPASE, RAS SUPER 2 FAMILY
1114	lmbl		49	222	1.2e-54			77.42	RAC1; CHAIN: NULL;	GTP-BINDING GTP-BINDING, GTPASE, SMALL G-PROTEIN, RHO
1114	lhrp	C	47	231	3.4e-51			89.47	RAN; CHAIN: A, C; NUCLEAR PORE COMPLEX PROTEIN NUP358; CHAIN: B, D;	COMPLEX (SMALL GTPASE/NUCLEAR PROTEIN) COMPLEX (SMALL GTPASE/NUCLEAR PROTEIN), SMALL GTPASE, 2 NUCLEAR

SEQ NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Fsi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1114	1x84	B	51	216	1.4e-51			70.72	P50-RHO GTP-CHAIN: A; TRANSFORMING PROTEIN RHOA; CHAIN: B;	TRANSPORT COMPLEX (GTPASE ACTIVATING PROTEIN-ONCOGENE) GTPASE-ACTIVATING PROTEIN RHO GTPASE RHO GTPASE ACTIVATION/PROTO-ONCOGENE, GTPASE, 2 TRANSITION STATE, GAP COMPLEX (GTP- BINDING/EFFECTOR) RAS-RELATED PROTEIN RAB3A; COMPLEX (GTP- BINDING/EFFECTOR), G PROTEIN, EFFECTOR, RABCD, 2 SYNAPTIC EXOCYTOSIS, RAB PROTEIN, RAB3A, RABPHILIN HYDROLASE: CDC42/CDC42GAP; CDC42/CDC42GAP; TRANSITION STATE, G-PROTEIN, GAP, CDC42, ALF3, HYDROLASE
1114	1zbd	A	49	226	1.7e-63			93.30	RAB-3A; CHAIN: A; RABPHILIN-3A; CHAIN: B;	HYDROLASE G PROTEIN, VESICULAR TRAFFICKING, GTP HYDROLYSIS, RAB 2 PROTEIN, NEUROTRANSMITTER RELEASE, HYDROLASE
1114	2u9r	A	50	230	3.4e-50			77.06	GTP BINDING PROTEIN (G25K); CHAIN: A; GTPASE ACTIVATING PROTEIN (RHO); CHAIN: B;	HYDROLASE G PROTEIN, VESICULAR TRAFFICKING, GTP HYDROLYSIS, RAB 2 PROTEIN, NEUROTRANSMITTER RELEASE, HYDROLASE
1114	3rab	A	47	221	6.8e-65			102.45	RAB3A; CHAIN: A;	HYDROLASE G PROTEIN, VESICULAR TRAFFICKING, GTP HYDROLYSIS, RAB 2 PROTEIN, NEUROTRANSMITTER RELEASE, HYDROLASE
1116	2bnh		2	324	1.7e-52			56.47	RIBONUCLEASE INHIBITOR; CHAIN: NULL;	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS
1120	5pnt		2	140	1.4e-54			214.70	LOW MOLECULAR WEIGHT PHOSPHOTYROSYL PHOSPHATASE; CHAIN: NULL;	HYDROLASE ORTHOPHOSPHORIC MONOESTER PHOSPHOHYDROLASE, HYDROLASE, ACETYLATION, TYROSINE PHOSPHATASE

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
1122	1av1	A	83	280	5.1e-05			51.65	APOLIPOPROTEIN A-I; CHAIN: A, B, C, D;	LIPID TRANSPORT APO A-I; LIPOPROTEIN LIPID TRANSPORT, CHOLESTEROL METABOLISM, 2 ATHEROSCLEROSIS, HDL, LCAT- ACTIVATION
1127	1a0l	A	465	741	3.4e-76			100.75	BETA-TRYPTASE; CHAIN: A, B, C, D;	SERINE PROTEINASE TRYPSIN-LIKE SERINE PROTEINASE, TETRAMER, HEPARIN, ALLERGY, 2 ASTHMA
1127	1a5i	A	454	739	5.1e-67			106.52	PLASMINOGEN ACTIVATOR; CHAIN: A; GLU-GLY-ARG CHLOROMETHYL KETONE; CHAIN: I;	COMPLEX (SERINE PROTEASE/INHIBITOR) (DELTA FEKQDSPAALPHA1; EGRCMK; SERINE PROTEASE, FIBRINOLYTIC ENZYMES, PLASMINOGEN 2 ACTIVATORS
1127	1aht	H	465	744	1.5e-73			91.53	ALPHA-THROMBIN; 1AHT 4 CHAIN: L, H; 1AHT 5 THIRUGEN; 1AHT 8 CHAIN: I; 1AHT 9	COMPLEX (SERINE PROTEINASE/INHIBITOR)
1127	1aut	C	464	739	5.1e-68			96.33	ACTIVATED PROTEIN C; CHAIN: C, L; D-PIE-PRO-MAI; CHAIN: P;	COMPLEX (BLOOD COAGULATION/INHIBITOR) AUTOPROTHROMBIN IIA; HYDROLASE, SERINE PROTEINASE, PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD COAGULATION/INHIBITOR)
1127	1aeb	B	468	739	1.7e-76			89.82	ENTEROPEPTIDASE; CHAIN: A; ENTEROPEPTIDASE; CHAIN: B; VAL-ASP-ASP-ASP-ASP-LYS PEPTIDE; CHAIN: C;	HYDROLASE/HYDROLASE INHIBITOR ENTEROKINASE, HEAVY CHAIN; ENTEROKINASE, LIGHT CHAIN; ENTEROPEPTIDASE, TRYPSINOGEN ACTIVATION, 2 HYDROLASE/HYDROLASE INHIBITOR

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fsi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1127	1etr	H	465	745	1.5e-71			92.09	HYDROLASE(SERINE PROTEINASE) EPSILON-THROMBIN (E.C.3.4.21.5) NON-COVALENT COMPLEX WITH IETK 3 MQPA IETK 4	
1127	1fky	A	463	742	1.4e-76			89.40	COAGULATION FACTOR XA-TRYPSIN CHIMERA; CHAIN: A; D-PHE-PRO-ARG-CHLOROMETHYLKETONE (PPACK) WITH CHAIN: I;	COMPLEX (PROTEASE/INHIBITOR) TRYPSIN, COAGULATION FACTOR XA, CHIMERA, PROTEASE, PPACK, 2 CHLOROMETHYLKETONE, COMPLEX (PROTEASE/INHIBITOR)
1127	1kig	H	465	745	3.4e-70			98.96	FACTOR XA; CHAIN: H, L; ANTICOAGULANT PEPTIDE; CHAIN: I;	COMPLEX (PROTEASE/INHIBITOR) RTAP; GLYCOPROTEIN, SERINE PROTEASE, PLASMA, BLOOD COAGULATION, 2 COMPLEX (PROTEASE/INHIBITOR)
1127	1mxx	K	425	739	1.7e-72			93.49	ALPHA-THROMBIN; CHAIN: L, H; PRETHROMBIN-2; CHAIN: K;	COMPLEX (BLOOD COAGULATION/PROENZYME) COMPLEX (BLOOD COAGULATION/PROENZYME), THROMBIN, 2 PRETHROMBIN-2, PLASMA, SERINE PROTEASE
1127	1pyt	D	454	739	1.5e-75			95.69	PROCARBOXYPEPTIDASE A; CHAIN: A, B; PROPROTEINASE E; CHAIN: C; CHYMOTRYPSINOGEN C; CHAIN: D;	TERNARY COMPLEX (ZYMOGEN) TC, PCPA-TC; TERNARY COMPLEX (ZYMOGEN), SERINE PROTEINASE, C-TERMINAL 2 PEPTIDASE
1127	1rnf	B	467	740	1.7e-68			102.89	TWO CHAIN TISSUE PLASMINOGEN ACTIVATOR; CHAIN: A, B;	SERINE PROTEASE (TC)-T-PA; SERINE PROTEASE, FIBRINOLYTIC ENZYMES
1135	1mcy	C	342	430	6.8e-47			71.69	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX

SEQ ID NO:	PDB ID	CHAIN ID	STAR T.AA	END AA	Pst Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1135	1t5	A	342	433	1.5e-21			67.88	TRANSCRIPTION FACTOR IIIA; CHAIN: A; 5S RNA GENE; CHAIN: E; F;	(ZINC FINGER/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA) TFIIIA; 5S GENE; NMR, TFIIIA, PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA 2 GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCRIPTION REGULATION/DNA)
1135	1t6	A	276	454	3.4e-41			105.09	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA) RNA POLYMERASE III, 2 (TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1135	1ubd	C	277	400	1.7e-30			80.44	YY1; CHAIN: C; ADENOVIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1135	2gli	A	277	431	1.4e-60			202.77	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1139	1mab	B	1	183	1.7e-46			64.40	FI-ATPASE ALPHA CHAIN; CHAIN: A; FI-ATPASE BETA CHAIN; CHAIN: B; FI-ATPASE GAMMA CHAIN; CHAIN: G;	HYDROLASE ATP SYNTHASE, FOPI-ATPASE, OXIDATIVE PHOSPHORYLATION, 2 MITOCHONDRIA, HYDROLASE

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1140	1mbb	B	51	264	6.8e-66			130.11	FI-ATPASE ALPHA CHAIN; CHAIN: A; FI-ATPASE BETA CHAIN: B; FI-ATPASE GAMMA CHAIN: C; G;	HYDROLASE ATP SYNTHASE, FO1-ATPASE, OXIDATIVE PHOSPHORYLATION, 2 MITOCHONDRIA, HYDROLASE
1148	1grz	A	3	122	1.6e-09	0.19	0.17		TOLB PROTEIN; CHAIN: A;	TOXIN BINDING PROTEIN TWO DOMAINS: BETA PROPELLER AND ALPHA/BETA FOLD
1148	1erj	A	11	127	3.2e-29	0.70	0.94		TRANSCRIPTIONAL REPRESSOR TUP1; CHAIN: A, B, C;	TRANSCRIPTION INHIBITOR BETA-PROPELLER
1148	1erj	A	3	79	3.2e-10	0.16	0.18		TRANSCRIPTIONAL REPRESSOR TUP1; CHAIN: A, B, C;	TRANSCRIPTION INHIBITOR BETA-PROPELLER
1148	1got	B	6	122	8e-22	0.01	0.40		GT-ALPHA/GALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION
1149	1erl	A	43	326	1.4e-97	0.69	1.00		MOESIN; CHAIN: A, B; MOESIN; CHAIN: C, D;	MEMBRANE PROTEIN CRYSTAL STRUCTURE, MEMBRANE, FERM DOMAIN, TAIL DOMAIN
1153	1a06		36	339	0			329.67	CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE; CHAIN: NULL;	KINASE KINASE, SIGNAL TRANSDUCTION, CALCIUM/CALMODULIN
1153	1a06		6	334	0	0.64	1.00		CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE; CHAIN: NULL;	KINASE KINASE, SIGNAL TRANSDUCTION, CALCIUM/CALMODULIN

SEQ NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1155	1cfe		51	203	1e-28			82.01	PATHOGENESIS-RELATED PROTEIN P14A; CHAIN: NULL;	PATHOGENESIS-RELATED PROTEIN P14A; CHAIN: NULL;
										PATHOGENESIS-RELATED LEAF PROTEIN 6, ETHYLENE PATHOGENESIS-RELATED PROTEIN, PR-1 PROTEINS, 2 PLANT DEFENSE
1155	1cfe		52	203	1e-28	0.47	1.00		PATHOGENESIS-RELATED PROTEIN P14A; CHAIN: NULL;	PATHOGENESIS-RELATED PROTEIN P14A; CHAIN: NULL;
										PATHOGENESIS-RELATED LEAF PROTEIN 6, ETHYLENE PATHOGENESIS-RELATED PROTEIN, PR-1 PROTEINS, 2 PLANT DEFENSE
1156	1ds6	A	1	96	1.2e-46	0.06	1.00		RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 2; CHAIN: A; RHO GDP-DISSOCIATION INHIBITOR 2; CHAIN: B;	SIGNALING PROTEIN P21-RAC2; RHO GDI 2, RHO-GDI BETA, LY-GDI; BETA SANDWICH, PROTEIN-PROTEIN COMPLEX; G-DOMAIN, 2 IMMUNOGLOBULIN FOLD; WALKER FOLD, GTP-BINDING PROTEIN
1159	1q19	A	23	239	1.5e-19	-0.03	0.62		URIDYLMONOPHOSPHATE/CYTIDYLMONOPHOSPHATE KINASE; CHAIN: A;	KINASE UMP/CMK KINASE; NUCLEOSIDE MONOPHOSPHATE KINASE, NMP KINASE, PHOSPHORYL 2 TRANSFER, TRANSITION STATE ANALOG COMPLEX, TRANSFERASE
1159	1q1f	A	249	424	5.1e-47	0.47	1.00		PHOSPHOGLYCERATE MUTASE; CHAIN: A, B;	TRANSFERASE TRANSFERASE (PHOSPHORYL)
1159	1q1f	A	250	449	5.1e-47			63.00	PHOSPHOGLYCERATE MUTASE; CHAIN: A, B;	TRANSFERASE TRANSFERASE (PHOSPHORYL)
1159	3adk		36	236	3.4e-26	-0.17	0.68		TRANSFERASE/PHOSPHOTRANSFERASE ADENYLATE KINASE (E.C.2.7.4.3) 3ADK 4	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
1159	3pgn		249	441	1.7e-48	0.19	1.00		TRANSFERASE (PHOSPHORYL) PHOSPHOGLYCERATE MUTASE (E.C.2.7.5.3) DE- PHOSPHO ENZYME 3PGM 4	
1159	3pgn		249	441	1.7e-48			38.96	TRANSFERASE (PHOSPHORYL) PHOSPHOGLYCERATE MUTASE (E.C.2.7.5.3) DE- PHOSPHO ENZYME 3PGM 4	
1159	3mkk	A	34	237	1.2e-29	-0.13	0.19		THYMIDYLATE KINASE; CHAIN: A, B, C, D, E, F, G, H;	KINASE KINASE, PHOSPHOTRANSFERASE
1160	1mey	C	360	442	4.8e-51			100.83	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1160	1rf6	A	276	437	8e-38			108.88	TITILIA; CHAIN: A, D; S5 RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1160	1ubd	C	334	442	5.1e-53			86.63	YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1160	2gji	A	304	443	3.2e-34			98.31	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fsi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
										BINDING PROTEIN/DNA
1163	1a06		43	340	3.2e-84			130.42	CALCULUM/CALMODULIN-DEPENDENT PROTEIN KINASE; CHAIN: NULL;	KINASE KINASE, SIGNAL TRANSDUCTION, CALCIUM/CALMODULIN
1163	1a60		18	334	6.8e-54			108.45	PROTEIN KINASE CK2/ALPHA-SUBUNIT; CHAIN: NULL;	TRANSFERASE TRANSFERASE, SERINE/THREONINE-PROTEIN KINASE, CASEIN KINASE, 2 SER/THR KINASE
1163	1apm	E	18	353	0			163.38	TRANSFERASE/PHOSPHOTRANSFERASE) SC-AMPS-DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (SCAPK5) 1APM 3 (CATALYTIC SUBUNIT) ALPHA ISOENZYME MUTANT WITH SER 139 1APM 4 REPLACED BY ALA (S139A) COMPLEX WITH THE PEPTIDE 1APM 5 INHIBITOR PKC3-24) AND THE DETERGENT MEGA-8 1APM 6	
1163	1aq1		50	348	4.8e-56			111.26	CYCLIN-DEPENDENT PROTEIN KINASE 2; CHAIN: NULL;	PROTEIN KINASE CDK2; PROTEIN KINASE, CELL CYCLE, PHOSPHORYLATION, STAUROSPORINE, 2 CELL DIVISION, MITOSIS, INHIBITION
1163	1b18	A	51	323	6.8e-56			95.00	CYCLIN-DEPENDENT KINASE 6; CHAIN: A, C; CYCLIN-DEPENDENT KINASE INHIBITOR; CHAIN: B, D;	CDK6; P19INK4D; CYCLIN DEPENDENT KINASE, CYCLIN DEPENDENT KINASE INHIBITORY 2 PROTEIN, CDK, INK4, CELL CYCLE, COMPLEX (KINASE/INHIBITOR) HEADER HELIX
1163	1bb	A	47	331	6.8e-62			113.75	CYCLIN-DEPENDENT KINASE 5; CHAIN: A, P19INK4D; CHAIN:	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR

SEQ NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									B;	PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1163	1byg	A	44	300	1.3e-31			93.49	C-TERMINAL SRC KINASE; CHAIN: A;	TRANSFERASE C5C; PROTEIN KINASE, C-TERMINAL SRC KINASE, PHOSPHORYLATION, 2 STAUROSPIRINE, TRANSFERASE
1163	1cmk	E	9	353	0			175.36	PHOSPHOTRANSFERASE CAMP-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT 1CMK 3 (E.C.2.7.1.37) 1CMK 4	
1163	1cjp	E	15	343	0			168.10	TRANSFERASE/PHOSPHOTRANSFERASE CAMP-DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (CAPK) 1CTP 3 (CATALYTIC SUBUNIT) 1CTP 4	
1163	1fgk	A	39	309	6.4e-31			105.44	FGF RECEPTOR 1; CHAIN: A, B;	PHOSPHOTRANSFERASE FGFRIK, FIBROBLAST GROWTH FACTOR RECEPTOR 1; TRANSFERASE, TYROSINE-PROTEIN KINASE, ATP-BINDING, 2 PHOSPHORYLATION, RECEPTOR, PHOSPHOTRANSFERASE
1163	1fgk	B	36	304	1.3e-37			117.87	FGF RECEPTOR 1; CHAIN: A, B;	PHOSPHOTRANSFERASE FGFRIK, FIBROBLAST GROWTH FACTOR RECEPTOR 1; TRANSFERASE, TYROSINE-PROTEIN KINASE, ATP-BINDING, 2 PHOSPHORYLATION, RECEPTOR, PHOSPHOTRANSFERASE
1163	1hel		50	348	1e-66			128.78	HUMAN CYCLIN-DEPENDENT KINASE 2; CHAIN: NULL;	PHOSPHOTRANSFERASE PROTEIN KINASE CDK2; TRANSFERASE, SERINE/THREONINE PROTEIN

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1163	1hr3	A	38	323	3.2e-26			99.07	INSULIN RECEPTOR; CHAIN: A; PEPTIDE SUBSTRATE; CHAIN: B;	KINASE, ATP-BINDING, 2 CELL CYCLE, CELL DIVISION, MITOSIS, PHOSPHORYLATION
										COMPLEX (TRANSFERASE/SUBSTRATE) TYROSINE KINASE, SIGNAL TRANSDUCTION, PHOSPHOTRANSFERASE, 2 COMPLEX (KINASE/PEPTIDE SUBSTRATE/ATP ANALOG), ENZYME, 3 COMPLEX (TRANSFERASE/SUBSTRATE)
1163	1jnk		38	388	5.1e-64			104.42	C-JUN N-TERMINAL KINASE; CHAIN: NULL;	TRANSFERASE JNK3; TRANSFERASE, JNK3 MAP KINASE, SERINE/THREONINE PROTEIN 2 KINASE
1163	1kob	A	24	359	1e-90			159.16	TWITCHIN; CHAIN: A, B;	KINASE KINASE, TWITCHIN, INTRASTERIC REGULATION
1163	1p28		31	395	1.6e-50			109.88	MAP KINASE P38; CHAIN: NULL;	TRANSFERASE MITOGEN ACTIVATED PROTEIN KINASE; TRANSFERASE, MAP KINASE, SERINE/THREONINE-PROTEIN KINASE, 2 P38
1163	1phk		49	305	1.1e-83			156.26	PHOSPHORYLASE KINASE; CHAIN: NULL;	KINASE RABBIT MUSCLE PHOSPHORYLASE KINASE; GLYCOGEN METABOLISM, TRANSFERASE, SERINE/THREONINE-PROTEIN, 2 KINASE, ATP-BINDING, CALMODULIN-BINDING
1163	1pme		44	389	9.6e-46			104.21	ERK2; CHAIN: NULL;	TRANSFERASE MAP KINASE, SERINE/THREONINE PROTEIN KINASE, TRANSFERASE
1163	1td1	A	47	370	8e-57			131.84	TITIN; CHAIN: A, B;	SERINE KINASE SERINE KINASE,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1163	3erk		36	460	3.4e-69			116.38	EXTRACELLULAR REGULATED KINASE 2; CHAIN: NULL;	TITIN, MUSCLE, AUTOINHIBITION TRANSFERASE MITOGEN ACTIVATED PROTEIN KINASE, MAP 2, ERK2; TRANSFERASE, SERINE/THREONINE-PROTEIN KINASE, MAP KINASE, 2 ERK2
1170	1bw m	A	17	247	1.6e-12			50.07	ALPHA-BETA T CELL RECEPTOR (TCR) (D10); CHAIN: A;	IMMUNE SYSTEM IMMUNOGLOBULIN, IMMUNORECEPTOR, IMMUNE SYSTEM
1170	1cdy		22	190	0.00034			50.90	T-CELL SURFACE GLYCOPROTEIN CD4; CHAIN: NULL;	T-CELL SURFACE GLYCOPROTEIN IMMUNOGLOBULIN FOLD, TRANSMEMBRANE, GLYCOPROTEIN, T-CELL, 2 MHC, LIPOPROTEIN, T-CELL SURFACE GLYCOPROTEIN
1170	1f58	H	17	244	4.8e-21			51.50	IGG1 ANTIBODY 58.2 (LIGHT CHAIN); CHAIN: L; IGG1 ANTIBODY 58.2 (HEAVY CHAIN); CHAIN: H; EXTERIOR MEMBRANE GLYCOPROTEIN (GP120); CHAIN: P;	IMMUNE SYSTEM FAB 58.2; FAB 58.2; V3 LOOP; IMMUNOGLOBULIN, FAB, HIV-1, GP120, V3, IMMUNE SYSTEM
1170	1fig	H	17	239	8e-19			51.43	IMMUNOGLOBULIN G1 (KAPPA LIGHT CHAIN) FAB' FRAGMENT, FIG 3	
1170	1qum	D	14	219	6.4e-23			50.17	MHC CLASS IIHLA-A; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; TAX PEPTIDE P6A; CHAIN: C; HMAN T-CELL RECEPTOR; CHAIN: D; IHLA-A 0201; CHAIN: E;	IMMUNE SYSTEM HUMAN TCRPEPTIDEMHC COMPLEX, HLA-A2, HTLV-1, TAX, TCR, T 2 CELL RECEPTOR, IMMUNE SYSTEM

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SFQFOL D score	Compound	PDB annotation
1170	2gfb	A	15	240	1.6e-17			51.08	IMMUNOGLOBULIN IGG2A FAB FRAGMENT (CNI206) 2GFB 3	IMMUNOGLOBULIN
1170	2pqp	B	17	239	9.6e-21			51.13	IMMUNOGLOBULIN; CHAIN: A, B, C, D;	IMMUNOGLOBULIN
1174	1a17		152	245	0.0017	-0.20	0.04		SERINE/THREONINE PROTEIN PHOSPHATASE 3; CHAIN: NULL;	HYDROLASE TETRATRICOPETIDE, TRP, HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE
1180	1f1b		195	418	1.7e-53			129.15	GAMMA-FIBRINOGEN CARBOXYL TERMINAL FRAGMENT; CHAIN: NULL;	BLOOD COAGULATION FACTOR BLOOD COAGULATION, GLYCOPROTEIN, CALCIUM, PLATELET, PLASMA, 2 ALTERNATIVE SPLICING, SIGNAL, DISEASE MUTATION, 3 POLYMORPHISM
1180	1fze	B	148	416	1.7e-63			132.32	FIBRIN; CHAIN: A, B, C, D, E, F, G, H, I, J;	BLOOD COAGULATION BLOOD COAGULATION, PLASMA PROTEIN, CROSSLINKING
1180	1fze	C	151	422	3.4e-62			141.90	FIBRIN; CHAIN: A, B, C, D, E, F, G, H, I, J;	BLOOD COAGULATION BLOOD COAGULATION, PLASMA PROTEIN, CROSSLINKING
1180	1fzd	A	242	419	1.7e-57			154.36	FIBRINOGEN-420; CHAIN: A, B, C, D, E, F, G, H;	BLOOD COAGULATION BLOOD COAGULATION, FIBRINOGEN-420, ALPHAC DOMAIN, 2 FIBRINOGEN RELATED DOMAIN, GLYCOSYLATED PROTEIN
1180	1fzg	C	170	419	1.1e-39			141.24	FIBRINOGEN; CHAIN: A, B, C, D, E, F, S, T, M, N;	BLOOD COAGULATION BLOOD COAGULATION, PLASMA, PLATELET, FIBRINOGEN, FIBRIN
1180	1fzg	E	160	416	3.2e-39			130.27	FIBRINOGEN; CHAIN: A, B, C,	BLOOD COAGULATION BLOOD

SEQ NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									D, E, F, S, T, M, N;	COAGULATION, PLASMA, PLAQUELET, FIBRINOGEN, FIBRIN
1181	1fm		2	104	1.6e-43			145.02	MACROPHAGE MIGRATION INHIBITORY FACTOR; CHAIN: NULL;	CYTOKINE MACROPHAGE, INFLAMMATORY RESPONSE, CYTOKINE
1181	1gif	A	1	115	1.6e-52			180.54	GLYCOSYLATION-INHIBITING FACTOR; CHAIN: A, B, C;	CYTOKINE MACROPHAGE, INFLAMMATORY RESPONSE, CYTOKINE
1181	1mf	A	2	115	3.2e-52			170.94	MACROPHAGE MIGRATION INHIBITORY FACTOR; CHAIN: A, B, C;	CYTOKINE PHENYLPIRUVATE AUTOMERASE; CYTOKINE, MACROPHAGE, INFLAMMATORY RESPONSE, AUTOMERASE
1185	1d2n	A	195	450	1.2e-35			76.43	N-ETHYLMALEIMIDE-SENSITIVE FUSION PROTEIN; CHAIN: A;	HEXAMERIZATION DOMAIN, HEXAMERIZATION DOMAIN, ATPASE, TRANSPORT
1195	1a8y		382	723	4.8e-23			91.59	CALSEQUESTIN; CHAIN: NULL	CALCIUM-BINDING PROTEIN CALSEQUESTIN, CALCIUM-BINDING PROTEIN, SARCOPLASMIC 2 RETICULUM, RABBIT SKELETAL MUSCLE
1200	1ayz	A	31	190	3.2e-47			71.29	UBIQUITIN-CONJUGATING ENZYME RAD6; CHAIN: A, B, C;	UBIQUITIN CONJUGATION UBC2; UBIQUITIN CONJUGATION, UBIQUITIN-CONJUGATING ENZYME
1200	1e4z	D	47	191	9.6e-40			84.49	UBIQUITIN-PROTEIN LIGASE E3A; CHAIN: A, B, C; UBIQUITIN CONJUGATING ENZYME E2; CHAIN: D;	LIGASE E6AP; UBCH7; BILOBAL STRUCTURE, ELONGATED SHAPE, E3 UBIQUITIN LIGASE, E2 2 UBIQUITIN CONJUGATING ENZYME
1200	1qcc	A	44	193	3.2e-53			81.61	UBIQUITIN CONJUGATING ENZYME; CHAIN: A;	LIGASE UBIQUITIN, UBIQUITIN-CONJUGATING ENZYME, YEAST

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Fsi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1200	1u9a	A	24	193	1.6e-43			74.19	UBC9; CHAIN: NULL;	UBIQUITIN-CONJUGATING ENZYME UBIQUITIN- CONJUGATING ENZYME; UBIQUITIN-CONJUGATING ENZYME; UBIQUITIN-DIRECTED 2 PROTEOLYSIS, CELL CYCLE CONTROL, LIGASE
1200	2aak		31	193	3.2e-47			71.32	UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	UBIQUITIN CONJUGATION UBC1; UBIQUITIN CONJUGATION, LIGASE
1200	2e2c		26	193	1.4e-41			67.54	UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	UBIQUITIN CONJUGATION, UBIQUITIN CARRIER PROTEIN, THIOESTER 2 BOND, LIGASE
1200	2ue2		33	193	3.2e-43			64.54	UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	UBIQUITIN CONJUGATION UBC7; UBIQUITIN CONJUGATION, LIGASE, YEAST
1204	1awj		241	317	3.2e-15	-0.35	0.06		ITK; CHAIN: NULL;	TRANSFERASE IL-2-INDUCIBLE T- CELL KINASE; TRANSFERASE, REGULATORY INTRAMOLECULAR COMPLEX, KINASE
1204	1aww		250	319	1.1e-13	0.55	0.58		BRUTON'S TYROSINE KINASE; CHAIN: NULL;	TRANSFERASE ATK, AMGX1, BPK; TYROSINE KINASE, X-LINKED AGAMMAGLOBULINEMIA, XLA
1204	1bu1	A	258	318	4.8e-15	0.03	0.21		HEMOPOIETIC CELL KINASE; CHAIN: A, B, C, D, E, F;	TRANSFERASE TYROSINE-PROTEIN KINASE, TRANSFERASE, SIGNAL TRANSDUCTION, 2 SH3
1204	1efn	A	258	317	1.6e-17	0.12	0.82		FYN TYROSINE KINASE; CHAIN: A, C; HIV-1 NEF PROTEIN; CHAIN: B, D;	COMPLEX (SH3 DOMAIN/VIRAL ENHANCER) SRC-HOMOLOGY 3 DOMAIN; COMPLEX (SH3 DOMAIN/VIRAL ENHANCER), PROTO-ONCOGENE, 2 TRANSFERASE, TYROSINE-

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Binst	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										PROTEIN KINASE, PHOSPHORYLATION, 3 AIDS, MYRISTYLATION, GTP-BINDING, ATP-BINDING, SH3 DOMAIN, 4 SH2 DOMAIN, PPI HELIX, PXXP MOTIF
1204	1fyn	A	255	318	6.4e-19	0.52	0.58		PHOSPHOTRANSFERASE FYN; CHAIN: A; 3BP*2; CHAIN: B;	TRANSFERASE PROTO-ONCOGENE TYROSINE KINASE; PROTO-ONCOGENE, TRANSFERASE, TYROSINE-PROTEIN KINASE, 2 PHOSPHORYLATION, ATP-BINDING, MYRISTYLATION, SH3 DOMAIN, 3 COMPLEX (PHOSPHOTRANSFERASE/PEPTIDE)
1204	1gbr	A	260	322	4.8e-12	0.25	0.63		SIGNAL TRANSDUCTION PROTEIN GROWTH FACTOR RECEPTOR-BOUND PROTEIN 2 (GRB2, N-TERMINAL 1GBR 3 SH3 DOMAIN) COMPLEXED WITH SOS-A PEPTIDE 1GBR 4 (NMR, 29 STRUCTURES) 1GBR 5	
1204	1lno	C	259	316	1.3e-16	0.42	0.69		C-SRC; CHAIN: C; NL1 (MN7-MN2-MN1-PLPPLP); CHAIN: N;	COMPLEX (TRANSFERASE/PEPTIDE) SRC, SH3 DOMAIN, LIGANDS, NON-PEPTIDE ELEMENTS, 2 COMPLEX (TRANSFERASE/PEPTIDE)
1204	1qlv	A	257	318	4.8e-13	0.41	0.43		TYROSINE-PROTEIN KINASE BTK; CHAIN: A;	TYROSINE-PROTEIN KINASE BRUTONS TYROSINE KINASE, B CELL PROGENITOR KINASE, TRANSFERASE, TYROSINE-PROTEIN KINASE, PHOSPHORYLATION, 2 SH3 DOMAIN
1204	1stif	A	256	318	8e-19	0.39	0.31		PHOSPHOTRANSFERASE FYN	

SEQ ID NO;	PDB ID	CHAI ID	STAR T AA	END AA	Fsi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									PROTO-ONCOGENE TYROSINE KINASE (E.C.2.7.1.112) ISHF 3 (SH3 DOMAIN) ISHF 4	
1204	2abl		251	423	9.6e-28	0.04	-0.15		ABL TYROSINE KINASE; CHAIN: NULL;	TRANSFERASE TRANSFERASE, TYROSINE KINASE, SH3, SH2, ONCOPROTEIN
1204	4hck		255	318	3.2e-15	0.04	0.55		HEMATOPOIETIC CELL KINASE; CHAIN: NULL;	TRANSFERASE HCK; SH3, PROTEIN TYROSINE KINASE, SIGNAL TRANSDUCTION, 2 TRANSFERASE
1205	1oxy	A	38	98	0.0096	0.69	0.19		CYTOCHROME B5; CHAIN: A;	ELECTRON TRANSPORT HELIX, BETA-STRAND, ELECTRON TRANSPORT
1208	1cho	I	554	592	5.1e-07	-0.30	0.58		COMPLEX (SERINE PROTEINASE-INHIBITOR) ALPHA-CHYMOTRYPSIN (E.C.3.4.21.1) COMPLEX WITH TURKEY 1CHO 4 OVOMUCOID THIRD DOMAIN (OMTKY35) 1CHO 5	
1208	1ldt	L	559	587	1.7e-07	-0.23	0.86		TRYPSIN; CHAIN: T; TRYPTASE INHIBITOR; CHAIN: L;	COMPLEX (HYDROLASE-INHIBITOR) LDTI; COMPLEX (HYDROLASE-INHIBITOR), HYDROLASE INHIBITOR, 2 INFLAMMATION, TRYPTASE
1215	1ack8		356	410	3.4e-05	-0.15	0.05		CALMODULIN; CHAIN: NULL;	CALCIUM-BINDING PROTEIN CALMODULIN CERUM TRIC-DOMAIN, RESIDUES 1 - 75; CERUM-LOADED, CALCIUM-BINDING PROTEIN
1215	1c7w	A	349	410	6.8e-06	-0.50	0.23		CALCIUM VECTOR PROTEIN;	METAL BINDING PROTEIN CAVP;

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Ts Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1215	1cdm	A	356	418	3.4e-05	-0.48	0.09		CHAIN: A; CALCIUM-BINDING PROTEIN COMPLEXED WITH CALMODULIN-BINDING DOMAIN OF ICDM 3 CALMODULIN-DEPENDENT PROTEIN KINASE II ICDM 4 COMPLEX(SERINE)	EF-HAND FAMILY, CALCIUM BINDING PROTEIN, NMR
1215	1cho	I	39	84	5.1e-10	0.04	0.65		PROTEINASE-INHIBITOR) ALPHA-CHYMOTRYPSIN (E.C.3.4.21.1) COMPLEX WITH TURKEY ICHO 4 OVOMUCOID THIRD DOMAIN (OMTKY3S) ICHO 5	
1215	1dth	A	349	410	1.7e-05	-0.26	0.21		CARDIAC TROPONIN C; CHAIN: A;	STRUCTURAL PROTEIN HELIX-TURN-HELIX
1215	1dtr	A	348	414	1.4e-05	0.15	0.05		CALMODULIN; CHAIN: A;	METAL TRANSPORT CALMODULIN; HIGH RESOLUTION, DISORDER
1215	1ezg	A	226	305	3.2e-06	0.21	0.13		THERMAL HYSTERESIS PROTEIN ISOFORM YL-1; CHAIN: A, B;	ANTIFREEZE PROTEIN INSECT HYSTERESIS, TENEBRIO 2 MOLITOR, IODINATION, RIGHT-HANDED BETA-HELIX, TMAPP
1215	1f71	A	349	410	6.8e-05	0.10	0.69		CALMODULIN; CHAIN: A;	TRANSPORT PROTEIN CALCIUM BINDING, EF HAND, FOUR-HELIX BUNDLE
1215	1fak	L	236	302	4.8e-09	0.07	-0.19		BLOOD COAGULATION FACTOR VIIA; CHAIN: L; BLOOD COAGULATION FACTOR VIIA; CHAIN: H; SOLUBLE TISSUE FACTOR; CHAIN: T; 5L15; CHAIN: I;	BLOOD CLOTTING COMPLEX(SERINE) PROTEASE(COFACTOR/LIGAND) BLOOD COAGULATION, 2 SERINE PROTEASE, COMPLEX, CO-FACTOR, RECEPTOR ENZYME, 3 INHIBITOR, GLA, EGF, COMPLEX (SERINE 4

SEQ NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Fsi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1215	1mb	A	201	426	1.7e-28			71.86	BASEMENT MEMBRANE PROTEIN BM-40; CHAIN: A; B;	PROTEASE/COFACTOR/LIGAND); BLOOD CLOTTING
1215	1qit	A	348	419	6.8e-07	-0.05	0.01		EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE CHAIN: A;	EXTRACELLULAR MODULE OSTONECTIN SPARC, SECRETED PROTEIN ACIDIC AND EXTRACELLULAR MODULE, GLYCOPROTEIN, ANTI-ADHESIVE PROTEIN, 2 COLLAGEN BINDING, SITE-DIRECTED MUTAGENESIS, GLYCOSYLATED 3 PROTEIN MODRES
1215	1rro		348	410	3.4e-05	-0.37	0.19		CALCIUM-BINDING PROTEIN RAT ONCOMODULIN IRRO 3	GROWTH FACTOR EHI; EH DOMAIN, EPS15, EF-HAND, SOLUTION STRUCTURE, S100 PROTEIN
1215	1sgp	I	43	84	1.7e-08	0.67	0.55		STREPTOMYCIN GRISINUS PROTEINASE B; ISGP 6 CHAIN: E; ISGP 7 TURKEY OVOMUCOID INHIBITOR; ISGP 11 CHAIN: I; ISGP 12 SPARC; ISRA 4 CHAIN: NULL; ISRA 5	COMPLEX (SERINE PROTEASE/INHIBITOR) SGPB; ISGP 8 ALA18-OMTKY3; ISGP 14 SERINE PROTEINASE, PROTEIN INHIBITOR ISGP 25
1215	1sra		279	423	1.5e-38	0.43	0.72		SPARC; ISRA 4 CHAIN: NULL; ISRA 5	CALCIUM-BINDING PROTEIN BM-40, OSTONECTIN; ISRA 7 EXTRACELLULAR MATRIX PROTEIN ISRA 20
1215	1sra		279	426	1.5e-38			58.51	SPARC; ISRA 4 CHAIN: NULL; ISRA 5	CALCIUM-BINDING PROTEIN BM-40, OSTONECTIN; ISRA 7 EXTRACELLULAR MATRIX PROTEIN ISRA 20
1215	1xka	L	240	313	4.8e-09	0.09	-0.19		BLOOD COAGULATION FACTOR XA; CHAIN: L; C;	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Fsl Blast	Verify score	PMF score	SEQFOL D score	Coumpound	PDB annotation
1215	3ovo		40	84	1.7e-09	0.76	0.21		PROTEINASE INHIBITOR (KAZAL) OYOMUCOID THIRD DOMAIN CLEAVED RD: 30VO 3	GROWTH FACTOR LIKE DOMAIN
1215	5pal		348	410	3.4e-05	-0.11	0.13		CALCIUM-BINDING PROTEIN PARVALBUMIN (ALPHA LINEAGE) 5PAL 3	
1215	9wga A		112	286	3.2e-15	0.08	-0.19		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
1216	1a8a		1	217	3.2e-51	0.58	1.00		ANNEXIN V; CHAIN: NULL;	PHOSPHOLIPID ANALOG PLACENTAL ANTICOAGULANT PROTEIN; PHOSPHOLIPID ANALOG, CALCIUM BINDING PROTEIN, MEMBRANE 2 BINDING PROTEIN
1216	1a8a		1	217	3.2e-51			75.48	ANNEXIN V; CHAIN: NULL;	PHOSPHOLIPID ANALOG PLACENTAL ANTICOAGULANT PROTEIN; PHOSPHOLIPID ANALOG, CALCIUM BINDING PROTEIN, MEMBRANE 2 BINDING PROTEIN
1216	1ain		61	222	1e-68	0.23	1.00		CALCIUM/PHOSPHOLIPID BINDING ANNEXIN I 1AIN 3	
1216	1ain		61	223	1e-68			170.55	CALCIUM/PHOSPHOLIPID BINDING ANNEXIN I 1AIN 3	
1216	1ain		62	222	4.8e-67	-0.02	1.00		CALCIUM/PHOSPHOLIPID BINDING ANNEXIN I 1AIN 3	
1216	1ala		1	214	3.2e-53	0.42	1.00		CALCIUM/PHOSPHOLIPID- BINDING PROTEIN ANNEXIN V 1ALA 3	
1216	1ala		1	214	3.2e-53			75.25	CALCIUM/PHOSPHOLIPID- BINDING PROTEIN ANNEXIN V 1ALA 3	

SEQ NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Fsi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1216	1ann		11	215	9.6e-51	0.42	1.00		ANNEXIN IV; IANN 5 CHAIN: NULL; IANN 6	CALCIUM/PHOSPHOLIPID-BINDING PROTEIN 32.5 KD CALELECTRIN, ENDONEXIN I; IANN 7 32.5KD CALELECTRIN, ENDONEXIN I, LIPOCORTIN IV, IANN 12.2 CHROMOBINDIN IV, PROTEIN II IANN 13
1216	1ann		1	216	3.2e-67			68.51	ANNEXIN IV; IANN 5 CHAIN: NULL; IANN 6	CALCIUM/PHOSPHOLIPID-BINDING PROTEIN 32.5 KD CALELECTRIN, ENDONEXIN I; IANN 7 32.5KD CALELECTRIN, ENDONEXIN I, LIPOCORTIN IV, IANN 12.2 CHROMOBINDIN IV, PROTEIN II IANN 13
1216	1ann		62	219	3.2e-67	0.46	1.00		ANNEXIN IV; IANN 5 CHAIN: NULL; IANN 6	CALCIUM/PHOSPHOLIPID-BINDING PROTEIN 32.5 KD CALELECTRIN, ENDONEXIN I; IANN 7 32.5KD CALELECTRIN, ENDONEXIN I, LIPOCORTIN IV, IANN 12.2 CHROMOBINDIN IV, PROTEIN II IANN 13
1216	1ave		10	216	1.6e-50	0.24	1.00		ANNEXIN VI; CHAIN: NULL;	CALCIUM/PHOSPHOLIPID-BINDING PROTEIN P68, PROTEIN III, 67-KDA- CALCIMEDIN, LIPOCORTIN ANNEXIN, CALCIUM-BINDING, MEMBRANE-BINDING, 2 CALCIUM/PHOSPHOLIPID-BINDING PROTEIN
1216	1ave		5	221	9.6e-78	0.48	1.00		ANNEXIN VI; CHAIN: NULL;	CALCIUM/PHOSPHOLIPID-BINDING PROTEIN P68, PROTEIN III, 67-KDA- CALCIMEDIN, LIPOCORTIN ANNEXIN, CALCIUM-BINDING, MEMBRANE-BINDING, 2 CALCIUM/PHOSPHOLIPID-BINDING

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1216	1axn		4	216	9.6e-53	0.76	1.00		ANNEXIN III; IAXN 4 CHAIN: NULL; IAXN 5	PROTEIN CALCIUM/PHOSPHOLIPID-BINDING PROTEIN ANNEXIN FAMILY 1 AXN 14
1216	1axn		53	223	3.2e-67			84.90	ANNEXIN III; IAXN 4 CHAIN: NULL; IAXN 5	CALCIUM/PHOSPHOLIPID-BINDING PROTEIN ANNEXIN FAMILY 1 AXN 14
1216	1axn		59	222	3.2e-67	0.70	1.00		ANNEXIN III; IAXN 4 CHAIN: NULL; IAXN 5	CALCIUM/PHOSPHOLIPID-BINDING PROTEIN ANNEXIN FAMILY 1 AXN 14
1216	1hvd		1	212	1.1e-49			65.28	CALCIUM/PHOSPHOLIPID BINDING ANNEXIN V (LIPOCORTIN V, ENDONEXIN II, PLACENTAL IHDV 3 ANTICOAGULANT PROTEIN) (CALCIUM IONS ARE VISIBLE) MUTATION IHDV 4 WITH GLU 17 REPLACED BY GLY (E17G) IHDV 5	CALCIUM/PHOSPHOLIPID-BINDING PROTEIN ANNEXIN FAMILY 1 AXN 14
1217	1a8a		8	189	8e-39	0.64	1.00		ANNEXIN V; CHAIN: NULL;	PHOSPHOLIPID ANALOG PLACENTAL ANTICOAGULANT PROTEIN; PHOSPHOLIPID ANALOG, CALCIUM BINDING PROTEIN, MEMBRANE 2 BINDING PROTEIN
1217	1ain		13	187	8e-32	0.22	1.00		CALCIUM/PHOSPHOLIPID BINDING ANNEXIN I IAIN 3	
1217	1ain		33	304	0			403.43	CALCIUM/PHOSPHOLIPID BINDING ANNEXIN I IAIN 3	
1217	1ain		35	300	0	0.17	1.00		CALCIUM/PHOSPHOLIPID BINDING ANNEXIN I IAIN 3	
1217	1aia		8	186	3.2e-38	0.31	1.00		CALCIUM/PHOSPHOLIPID- BINDING PROTEIN ANNEXIN V IALA 3	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T.A.A.	END A.A.	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1217	1ann		8	187	3.2e-38	0.55	1.00		ANNEXIN IV; IANN 5 CHAIN: NULL; IANN 6	CALCIUM/PHOSPHOLIPID-BINDING PROTEIN 32.5 KD CALELECTRIN, ENDONEXIN I; IANN 7 32.5KD CALELECTRIN, ENDONEXIN I, LIPOCORTIN IV, IANN 12 2 CHROMOBINDIN IV, PROTEIN II IANN 13
1217	1avc		8	186	4.8e-26	0.28	1.00		ANNEXIN VI; CHAIN: NULL;	CALCIUM/PHOSPHOLIPID-BINDING PROTEIN P68, PROTEIN III, 67-KDA-CALCIMEDIN, LIPOCORTIN ANNEXIN; CALCIUM-BINDING, MEMBRANE-BINDING, 2
1217	1axn		8	187	1.6e-37	0.54	1.00		ANNEXIN III; IAXN 4 CHAIN: NULL; IAXN 5	CALCIUM/PHOSPHOLIPID-BINDING PROTEIN ANNEXIN FAMILY 1 AXN 14
1217	1lhd		8	184	6.4e-38	0.31	1.00		CALCIUM/PHOSPHOLIPID BINDING ANNEXIN V (LIPOCORTIN V, ENDONEXIN II, PLACENTAL IHVD 3 ANTICOAGULANT PROTEIN) (CALCIUM IONS ARE VISIBLE) MUTATION IHVD 4 WITH GLU 17 REPLACED BY GLY (E17G) IHVD 5	
1218	1a8a		31	195	3.2e-66			58.84	ANNEXIN V; CHAIN: NULL;	PHOSPHOLIPID ANALOG PLACENTAL ANTICOAGULANT PROTEIN; PHOSPHOLIPID ANALOG, CALCIUM BINDING PROTEIN, MEMBRANE 2 BINDING PROTEIN
1218	1a8a		33	194	3.2e-66	0.68	1.00		ANNEXIN V; CHAIN: NULL;	PHOSPHOLIPID ANALOG PLACENTAL ANTICOAGULANT

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Fgi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										PROTEIN: PHOSPHOLIPID ANALOG, CALCIUM BINDING PROTEIN, MEMBRANE 2 BINDING PROTEIN
1218	1ain		33	194	1e-68	0.23	1.00		CALCIUM/PHOSPHOLIPID BINDING ANNEXIN I IAIN 3	
1218	1ain		33	195	1e-68			170.39	CALCIUM/PHOSPHOLIPID BINDING ANNEXIN I IAIN 3	
1218	1ain		35	194	1.6e-65	0.15	1.00		CALCIUM/PHOSPHOLIPID BINDING ANNEXIN I IAIN 3	
1218	1ann		33	195	3.2e-68			65.05	ANNEXIN IV; IANN 5 CHAIN: NULL; IANN 6	CALCIUM/PHOSPHOLIPID-BINDING PROTEIN 32.5 KD CALECTRIN, ENDONEXIN I, CALECTRIN, ENDONEXIN I, LIPOCORTIN IV, IANN 12.2, CHROMOBINDIN IV, PROTEIN II IANN 13
1218	1ann		34	190	3.2e-68	0.54	1.00		ANNEXIN IV; IANN 5 CHAIN: NULL; IANN 6	CALCIUM/PHOSPHOLIPID-BINDING PROTEIN 32.5 KD CALECTRIN, ENDONEXIN I; IANN 7 32.5KD CALECTRIN, ENDONEXIN I, LIPOCORTIN IV, IANN 12.2 CHROMOBINDIN IV, PROTEIN II IANN 13
1218	1ave		2	186	1.6e-38	0.30	1.00		ANNEXIN VI; CHAIN: NULL;	CALCIUM/PHOSPHOLIPID-BINDING PROTEIN P68, PROTEIN III, 67-KDA-CALCIMEDIN, LIPOCORTIN ANNEXIN, CALCIUM-BINDING, MEMBRANE-BINDING, 2 CALCIUM/PHOSPHOLIPID-BINDING PROTEIN
1218	1ave		34	193	1.6e-71	0.61	1.00		ANNEXIN VI; CHAIN: NULL;	CALCIUM/PHOSPHOLIPID-BINDING PROTEIN P68, PROTEIN III, 67-KDA-CALCIMEDIN, LIPOCORTIN ANNEXIN, CALCIUM-BINDING,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
										MEMBRANE-BINDING, 2 CALCIUM/PHOSPHOLIPID-BINDING PROTEIN
1218	1axn		25	195	6.4e-67			85.90	ANNEXIN III; 1AXN 4 CHAIN; NULL; 1AXN 5	CALCIUM/PHOSPHOLIPID-BINDING PROTEIN ANNEXIN FAMILY 1 AXN 14
1218	1axn		31	194	6.4e-67	0.70	1.00		ANNEXIN III; 1AXN 4 CHAIN; NULL; 1AXN 5	CALCIUM/PHOSPHOLIPID-BINDING PROTEIN ANNEXIN FAMILY 1 AXN 14
1218	1dx5	A	2	169	3.2e-19	0.02	1.00		ANNEXIN 24(CA32); CHAIN: A, B;	METAL BINDING PROTEIN PLANT ANNEXIN, CAPSICUM ANNUUM, BELL PEPPER, CALCIUM 2 BINDING PROTEIN
1218	1hvd		32	195	9.6e-68			68.02	CALCIUM/PHOSPHOLIPID BINDING ANNEXIN V (LIPOCORTIN V; ENDONEXIN II; PLACENTAL 1HVD 3 ANTICOAGULANT PROTEIN) (CALCIUM IONS ARE VISIBLE) MUTATION 1HVD 4 WITH GLU 17 REPLACED BY GLY (E17G) 1HVD 5	
1218	1hvd		33	194	9.6e-68	0.59	1.00		CALCIUM/PHOSPHOLIPID BINDING ANNEXIN V (LIPOCORTIN V; ENDONEXIN II; PLACENTAL 1HVD 3 ANTICOAGULANT PROTEIN) (CALCIUM IONS ARE VISIBLE) MUTATION 1HVD 4 WITH GLU 17 REPLACED BY GLY (E17G) 1HVD 5	
1219	1b3u	A	23	627	1.6e-45			120.36	PROTEIN PHOSPHATASE PP2A; CHAIN: A, B;	SCAFFOLD PROTEIN SCAFFOLD PROTEIN, PP2A,

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Fsi Blast	Verity score	PMF score	SEQFOL D score	Compound	PDB annotation
1219	1b3u	A	320	613	1.6e-09	0.07	0.23		PROTEIN PHOSPHATASE PP2A; CHAIN: A, B;	PHOSPHORYLATION, HEAT REPEAT SCAFFOLD PROTEIN SCAFFOLD PROTEIN, PP2A, PHOSPHORYLATION, HEAT REPEAT SCAFFOLD PROTEIN SCAFFOLD PROTEIN, PP2A,
1219	1b3u	A	71	625	1.6e-45	0.04	-0.07		PROTEIN PHOSPHATASE PP2A; CHAIN: A, B;	PHOSPHORYLATION, HEAT REPEAT SCAFFOLD PROTEIN SCAFFOLD PROTEIN, PP2A,
1219	1ee4	A	211	473	1.7e-10	0.36	1.00		KARYOPHERIN ALPHA; CHAIN: A, B; MYC PROTO-ONCOGENE PROTEIN; CHAIN: C, D, E, F;	PHOSPHORYLATION, HEAT REPEAT TRANSPORT PROTEIN SERINE-RICH RNA POLYMERASE I SUPPRESSOR PROTEIN; ARM REPEAT
1219	1ee4	A	279	643	1.4e-44	0.37	0.86		KARYOPHERIN ALPHA; CHAIN: A, B; MYC PROTO-ONCOGENE PROTEIN; CHAIN: C, D, E, F;	TRANSPORT PROTEIN SERINE-RICH RNA POLYMERASE I SUPPRESSOR PROTEIN; ARM REPEAT
1219	1lal	A	179	628	1.3e-43			118.96	IMPORTIN ALPHA; CHAIN: A;	NUCLEAR IMPORT RECEPTOR KARYOPHERIN ALPHA; NUCLEAR IMPORT RECEPTOR, NUCLEAR LOCALIZATION SIGNAL, 2 ARMADILLO REPEATS, AUTOINHIBITION, INTRASTERIC REGULATION
1219	1lal	A	272	643	1.3e-43	0.50	0.53		IMPORTIN ALPHA; CHAIN: A;	NUCLEAR IMPORT RECEPTOR KARYOPHERIN ALPHA; NUCLEAR IMPORT RECEPTOR, NUCLEAR LOCALIZATION SIGNAL, 2 ARMADILLO REPEATS, AUTOINHIBITION, INTRASTERIC REGULATION
1219	1lur	B	318	633	4.8e-15	0.01	-0.15		KAN; CHAIN: A, C; IMPORTIN BETA SUBUNIT; CHAIN: B, D;	SMALL GTPASE KARYOPHERIN BETA, P95 SMALL GTPASE, NUCLEAR TRANSPORT RECEPTOR STRUCTURAL PROTEIN
1219	2bet		239	643	1.1e-39	0.51	0.06		BETA-CATENIN; CHAIN: NULL;	ARMADILLO REPEAT, BETA-

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1219	3bet		277	643	3.2e-35	0.46	0.24		BETA-CATENIN; CHAIN: NULL; ARMADILLO REPEAT ARMADILLO CYTOSKELETON	CATENIN, STRUCTURAL PROTEIN
1221	1bu7	A	19	486	9.6e-53			174.17	CYTOCHROME P450; CHAIN: A; B;	OXIDOREDUCTASE FATTY ACID HYDROXYLASE; FATTY ACID MONOOXYGENASE, HEMOPROTEIN, P450 REMARK
1221	1oxa		27	486	3.2e-24			94.76	CYTOCHROME P450 ERYF; 10XA 5 CHAIN: NULL 10XA 6	OXIDOREDUCTASE (OXYGENASE)
1222	1bu7	A	35	324	1.3e-18	-0.20	0.04		CYTOCHROME P450; CHAIN: A; B;	OXIDOREDUCTASE FATTY ACID HYDROXYLASE; FATTY ACID MONOOXYGENASE, HEMOPROTEIN, P450 REMARK
1222	1bu7	A	61	318	3.4e-36	-0.23	0.29		CYTOCHROME P450; CHAIN: A; B;	OXIDOREDUCTASE FATTY ACID HYDROXYLASE; FATTY ACID MONOOXYGENASE, HEMOPROTEIN, P450 REMARK
1222	1dt6	A	31	325	3.2e-92	-0.02	0.99		CYTOCHROME P450 2CS; CHAIN: A;	OXIDOREDUCTASE PROGESTERONE 21-HYDROXYLASE, CYP11CS P450 1, MEMBRANE PROTEIN, PROGESTERONE 21-HYDROXYLASE, BENZO(A) 2 PYRENE HYDROXYLASE, ESTRADIOL 2-HYDROXYLASE, P450, CYP2C5
1222	1t26	A	48	318	1.7e-21	-0.08	0.05		NITRIC OXIDE REDUCTASE; CHAIN: A;	OXIDOREDUCTASE NITRIC OXIDE REDUCTASE, CYTOCHROME P450NOR
1222	1oxa		61	318	6.8e-33	-0.40	0.28		CYTOCHROME P450 ERYF; 10XA 5 CHAIN: NULL 10XA 6	OXIDOREDUCTASE (OXYGENASE)

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1227	1erz	A	130	352	0.00032	-0.06	0.04		TOLD PROTEIN; CHAIN: A;	TOXIN BINDING PROTEIN TWO DOMAINS: BETA PROPELLER AND ALPHA/BETA FOLD
1227	1erj	A	116	431	4.8e-73	0.57	1.00		TRANSCRIPTIONAL REPRESSOR TUP1; CHAIN: A; B, C;	TRANSCRIPTION INHIBITOR BETA-PROPELLER
1227	1erj	A	4	285	1.3e-58	0.40	0.29		TRANSCRIPTIONAL REPRESSOR TUP1; CHAIN: A; B, C;	TRANSCRIPTION INHIBITOR BETA-PROPELLER
1227	1erj	A	65	373	1.6e-66	0.38	1.00		TRANSCRIPTIONAL REPRESSOR TUP1; CHAIN: A; B, C;	TRANSCRIPTION INHIBITOR BETA-PROPELLER
1227	1got	B	12	370	1.3e-77			119.11	GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION
1227	1got	B	14	328	1.3e-77	0.14	0.53		GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION
1227	1got	B	166	431	4.8e-54	0.64	1.00		GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-

SEQ ID NO:	PDB ID	CHAIN ID	STAR T.AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										BINDING(TRANSDUCER), G PROTEIN, HETERODIMER 2 SIGNAL TRANSDUCTION
1235	1aif	H	413	518	0.0068	-0.14	0.35		ANTI-IDIDOTYPIC FAB 409.3.3 (GGGA) FAB; CHAIN: A, B, L, H	IMMUNOGLOBULIN C REGION, V REGION
1235	1qun	B	321	580	1.2e-15	-0.00	-0.18		PAPD-LIKE CHAPERONE FIMC; CHAIN: A, C, E, G, I, K, M, O; MANNOSE-SPECIFIC ADHESIN FIMH; CHAIN: B, D, F, H, J, L, N, P;	CHAPERONE/STRUCTURAL PROTEIN CHAPERONE ADHESIN DONOR STRAND COMPLEMENTATION, 2 CHAPERONE/STRUCTURAL PROTEIN
1235	1qun	B	408	701	6.8e-16	0.11	-0.19		PAPD-LIKE CHAPERONE FIMC; CHAIN: A, C, E, G, I, K, M, O; MANNOSE-SPECIFIC ADHESIN FIMH; CHAIN: B, D, F, H, J, L, N, P;	CHAPERONE/STRUCTURAL PROTEIN CHAPERONE ADHESIN DONOR STRAND COMPLEMENTATION, 2 CHAPERONE/STRUCTURAL PROTEIN
1236	1f52	A	214	293	0.00034	-0.25	0.13		SKP2; CHAIN: A, C; SKP1; CHAIN: B, D;	LIGASE CYCLIN A/CDK2-ASSOCIATED P45; CYCLIN A/CDK2-ASSOCIATED P19; SKP1, SKP2, F-BOX, LRRS, LEUCINE-RICH REPEATS, SCF, 2 UBIQUITIN, E3, UBIQUITIN PROTEIN LIGASE
1236	1pjr		430	960	3.2e-68	-0.22	0.58		PCRA; CHAIN: NULL;	HELICASE DNA REPAIR, DNA REPLICATION, SOS RESPONSE, HELICASE, 2 ATP-BINDING, DNA-BINDING
1236	1uan	A	441	872	1.6e-47	-0.55	0.00		ATP-DEPENDENT DNA HELICASE REP; CHAIN: A, B; DNA CHAIN: C;	COMPLEX (HELICASE/DNA) HELICASE (HELICASE/DNA), HELICASE, DNA UNWINDING
1236	2pjt	A	436	991	1.3e-62			90.62	HELICASE PCRA; CHAIN: A, F;	HYDROLASE/DNA ATP-DEPENDENT

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									HELICASE PCRA; CHAIN: B, G; DNA (5'-D(*Tp*Tp*Tp*T)-3'); CHAIN: C, D; DNA (5'-D(*Gp*G)-3'); CHAIN: E; DNA (5'-D(*Ap*CP*TP*Gp*G)-3'); CHAIN: F;	HELICASE PCRA: ATP-DEPENDENT HELICASE PCRA; HELICASE PCRA, HYDROLASE, DNA, PRODUCT COMPLEX
1237	1a4y	A	10	213	3.4e-22	-0.01	0.89		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPI TOPE MAPPING, LEUCINE-RICH 3 REPEATS
1237	1a4y	A	126	299	6.4e-07	0.04	0.09		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPI TOPE MAPPING, LEUCINE-RICH 3 REPEATS
1237	1a6n	A	12	151	3.4e-13	0.04	0.35		U2 RNA HAIRPIN IV; CHAIN: Q; R; U2 A'; CHAIN: A, C; U2 B'; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP RIBONUCLEOPROTEIN
1237	1a9n	A	20	101	3.2e-07	0.28	0.51		U2 RNA HAIRPIN IV; CHAIN: Q; R; U2 A'; CHAIN: A, C; U2 B'; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP RIBONUCLEOPROTEIN
1237	1a9n	A	51	187	8.5e-24	0.36	0.71		U2 RNA HAIRPIN IV; CHAIN: Q; R; U2 A'; CHAIN: A, C; U2 B'; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP RIBONUCLEOPROTEIN
1237	1a9n	A	72	196	3.4e-20	0.04	0.04		U2 RNA HAIRPIN IV; CHAIN: Q; R; U2 A'; CHAIN: A, C; U2 B'; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1237	1a9n	C	20	101	3.2e-07	0.49	0.35		U2 RNA HAIRPIN IV; CHAIN: Q; R: U2 A'; CHAIN: A, C; U2 B'; CHAIN: B, D;	SNRNP RIBONUCLEOPROTEIN COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP RIBONUCLEOPROTEIN
1237	1a9n	C	51	192	5.1e-24	0.05	0.66		U2 RNA HAIRPIN IV; CHAIN: Q; R: U2 A'; CHAIN: A, C; U2 B'; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP RIBONUCLEOPROTEIN
1237	1d0b	A	3	187	3.2e-25	-0.14	0.71		INTERNALIN B; CHAIN: A;	CELL ADHESION; LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1237	1d0b	A	44	221	6.8e-29	-0.20	0.07		INTERNALIN B; CHAIN: A;	CELL ADHESION; LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1237	1d0b	A	75	268	6.4e-21	0.15	-0.02		INTERNALIN B; CHAIN: A;	CELL ADHESION; LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1237	1dce	A	11	100	1.6e-11	0.35	0.96		RAB GERANYLGERANYLTRANSFERASE RASE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRANSFERASE BETA SUBUNIT; CHAIN: B, D;	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N-FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
1237	1dce	A	130	233	3.2e-13	0.47	0.94		RAB GERANYLGERANYLTRANSFERASE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRANSFERASE BETA SUBUNIT; CHAIN: B, D;	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N-FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
1237	1dce	A	160	278	4.8e-10	0.20	-0.03		RAB GERANYLGERANYLTRANSFERASE	TRANSFERASE CRYSTAL STRUCTURE, RAB

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									RASE ALPHA SUBUNIT; CHAIN: A, C, RAB GERANYLGERANYLTRANSFERASE RASE BETA SUBUNIT; CHAIN: B, D;	GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N- FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
1237	1dce	A	44	169	3.2e-11	0.21	0.33		RAB GERANYLGERANYLTRANSFERASE RASE ALPHA SUBUNIT; CHAIN: A, C, RAB GERANYLGERANYLTRANSFERASE RASE BETA SUBUNIT; CHAIN: B, D;	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N- FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
1237	1d69	A	11	146	4.8e-12	-0.31	0.09		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LUCINE- RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA
1237	1d69	A	130	252	3.2e-14	-0.20	0.22		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LUCINE- RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA
1237	1d69	A	37	169	1.6e-11	-0.54	0.45		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LUCINE- RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA
1237	1fo1	A	132	192	1.1e-06	-0.03	0.65		NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP, RBD OR RRM) AND LUCINE-RICH- REPEAT 2 (LRR)
1237	1fo1	B	132	192	1.1e-06	0.25	0.60		NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP, RBD OR RRM) AND LUCINE-RICH- REPEAT 2 (LRR)
1237	1f52	A	10	206	1.2e-25	0.15	0.16		SKP2, CHAIN: A, C, SKP1; CHAIN: B, D;	LIGASE CYCLIN AC/DK2- ASSOCIATED P45; CYCLIN A/C/DK2-

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										ASSOCIATED P19; SKP1, SKP2, F-BOX, LRRS, LEUCINE-RICH REPEATS, SCF, 2 UBIQUITIN, E3, UBIQUITIN PROTEIN LIGASE
1237	1f52	A	130	294	1.1e-06	0.34	0.22		SKP2; CHAIN: A, C, SKP1; CHAIN: B, D;	LIGASE CYCLIN ACDK2-ASSOCIATED P19; SKP1, SKP2, F-BOX, LRRS, LEUCINE-RICH REPEATS, SCF, 2 UBIQUITIN, E3, UBIQUITIN PROTEIN LIGASE
1237	2bah		19	223	1.5e-28	-0.03	0.82		RIBONUCLEASE INHIBITOR; CHAIN: NULL;	ACETYLATION KINASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS
1238	1a17		119	279	1e-18	0.10	0.80		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	HYDROLASE TETRA TRICOPEPTIDE, TRP, HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE
1238	1a17		133	250	6.4e-14	0.27	0.51		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	HYDROLASE TETRA TRICOPEPTIDE, TRP, HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE
1238	1a17		153	296	4.8e-13	0.30	0.76		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	HYDROLASE TETRA TRICOPEPTIDE, TRP, HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE
1238	1a17		20	153	8e-13	0.01	0.23		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	HYDROLASE TETRA TRICOPEPTIDE, TRP, HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1238	1a17		221	368	5.1e-19	0.31	0.99		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	STRUCTURE HYDROLASE TETRA TRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY
1238	1a17		212	348	9.6e-13	0.56	0.94		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	STRUCTURE HYDROLASE TETRA TRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY
1238	1a17		263	392	9.6e-13	0.22	0.80		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	STRUCTURE HYDROLASE TETRA TRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY
1238	1a17		290	416	3.2e-14	0.22	0.52		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	STRUCTURE HYDROLASE TETRA TRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY
1238	1a17		29	142	1.7e-15	0.18	0.11		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	STRUCTURE HYDROLASE TETRA TRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY
1238	1a17		300	414	1.7e-18	-0.14	0.74		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	STRUCTURE HYDROLASE TETRA TRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY
1238	1a17		338	421	4.8e-13	0.41	0.37		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	STRUCTURE HYDROLASE TETRA TRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1238	1al7		56	184	1.7e-15	0.18	0.70		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	TPR, 2 SUPER-HELIX, X-RAY STRUCTURE HYDROLASE TETRA TRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE
1238	1al7		63	175	8e-10	0.34	0.41		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	HYDROLASE TETRA TRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE
1238	1al7		85	209	4.8e-11	0.12	0.58		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	HYDROLASE TETRA TRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE
1238	1al7		89	212	3.4e-17	0.12	0.65		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	HYDROLASE TETRA TRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE
1238	1d8d	A	217	410	4.8e-07	-0.23	0.60		FARNESYLTRANSFERASE (ALPHA SUBUNIT); CHAIN: A; FARNESYLTRANSFERASE (BETA SUBUNIT); CHAIN: B; K-RAS4B PEPTIDE SUBSTRATE; CHAIN: P;	TRANSFERASE FTASE; FTASE; FTASE, PFT, PFTASE, FARNESYLTRANSFERASE, FARNESYL 2 TRANSFERASE, CAAX, RAS, CANCER
1238	1d8d	A	28	266	3.4e-15	-0.04	0.18		FARNESYLTRANSFERASE (ALPHA SUBUNIT); CHAIN: A; FARNESYLTRANSFERASE (BETA SUBUNIT); CHAIN: B; K-RAS4B PEPTIDE SUBSTRATE; CHAIN: P;	TRANSFERASE FTASE; FTASE, FTASE, PFT, PFTASE, FARNESYLTRANSFERASE, FARNESYL 2 TRANSFERASE, CAAX, RAS, CANCER

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1238	1e96	B	135	278	1.4e-09	0.15	0.48		RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 1; CHAIN: A; NEUTROPHIL CYTOSOL FACTOR 2 (NCF-2) CHAIN: B;	SIGNALLING COMPLEX RAC1; P67PHOX; SIGNALLING COMPLEX, GTPASE, NADPH OXIDASE, PROTEIN-PROTEIN 2 COMPLEX, TPR MOTIF
1238	1e96	B	189	322	8e-10	0.40	0.76		RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 1; CHAIN: A; NEUTROPHIL CYTOSOL FACTOR 2 (NCF-2) CHAIN: B;	SIGNALLING COMPLEX RAC1; P67PHOX; SIGNALLING COMPLEX, GTPASE, NADPH OXIDASE, PROTEIN-PROTEIN 2 COMPLEX, TPR MOTIF
1238	1e96	B	229	379	4.8e-09	0.14	0.98		RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 1; CHAIN: A; NEUTROPHIL CYTOSOL FACTOR 2 (NCF-2) CHAIN: B;	SIGNALLING COMPLEX RAC1; P67PHOX; SIGNALLING COMPLEX, GTPASE, NADPH OXIDASE, PROTEIN-PROTEIN 2 COMPLEX, TPR MOTIF
1238	1e96	B	290	417	4.8e-09	0.05	0.86		RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 1; CHAIN: A; NEUTROPHIL CYTOSOL FACTOR 2 (NCF-2) CHAIN: B;	SIGNALLING COMPLEX RAC1; P67PHOX; SIGNALLING COMPLEX, GTPASE, NADPH OXIDASE, PROTEIN-PROTEIN 2 COMPLEX, TPR MOTIF
1238	1e96	B	62	244	0.00016	0.12	0.21		RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 1; CHAIN: A; NEUTROPHIL CYTOSOL FACTOR 2 (NCF-2) CHAIN: B;	SIGNALLING COMPLEX RAC1; P67PHOX; SIGNALLING COMPLEX, GTPASE, NADPH OXIDASE, PROTEIN-PROTEIN 2 COMPLEX, TPR MOTIF
1238	1e1r	A	133	247	6.4e-15	0.38	0.47		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
1238	1e1r	A	161	252	6.4e-15	0.24	1.00		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
1238	1e1r	A	195	283	1.6e-10	0.02	0.96		TPR2A-DOMAIN OF HOP;	CHAPERONE HOP, TPR-DOMAIN,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
1238	1eir	A	228	326	4.8e-12	0.47	0.99		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
1238	1eir	A	262	355	3.2e-13	0.27	0.74		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
1238	1eir	A	28	117	4.8e-11	0.13	0.29		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
1238	1eir	A	334	419	4.8e-12	0.54	0.55		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
1238	1eir	A	93	185	1.1e-11	0.31	0.33		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
1238	1elw	A	135	221	1.1e-13	0.46	0.99		TPR1-DOMAIN OF HOP; CHAIN: A; B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
1238	1elw	A	155	262	1.3e-12	0.47	0.96		TPR1-DOMAIN OF HOP; CHAIN: A; B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
1238	1elw	A	196	296	3.2e-10	0.63	1.00		TPR1-DOMAIN OF HOP; CHAIN: A; B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING

SEQ NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1238	1elw	A	236	332	4.8e-13	0.76	1.00		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	BINDING CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
1238	1elw	A	25	122	4.8e-10	0.52	0.57		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
1238	1elw	A	2	99	6.4e-14	0.25	0.03		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
1238	1elw	A	304	408	3.2e-15	0.23	0.98		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
1238	1elw	A	342	419	1.1e-11	0.29	0.21		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
1238	1elw	A	61	155	6.4e-10	0.32	0.82		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
1238	1elw	A	166	413	9.6e-38	0.32	1.00		PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: C, D;	SIGNALING PROTEIN PEROXISOMAL RECEPTOR 1, PTS1-BP, PEROXIN-5, PTS1 PROTEIN-TETRAMERIC COMPLEX, TETRAMERIC PEPTIDE REPEAT, TPR, 2 HELICAL REPEAT
1238	1elw	A	313	420	3.2e-09	0.07	0.96		PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTS1-CONTAINING	SIGNALING PROTEIN PEROXISOMAL RECEPTOR 1, PTS1-BP, PEROXIN-5, PTS1 PROTEIN-TETRAMERIC COMPLEX, TETRAMERIC PEPTIDE REPEAT, TPR, 2 HELICAL REPEAT

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									PEPTIDE; CHAIN: C, D;	PEPTIDE COMPLEX, TETRATRICOPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT
1238	1fch	A	34	273	6.4e-31	0.48	1.00		PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: C, D;	SIGNALING PROTEIN PEROXISOMORE RECEPTOR 1, PTS1-BP, PEROXIN-5, PTS1 PROTEIN-PEPTIDE COMPLEX, TETRATRICOPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT
1238	1fch	A	7	220	1.3e-29	0.38	1.00		PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: C, D;	SIGNALING PROTEIN PEROXISOMORE RECEPTOR 1, PTS1-BP, PEROXIN-5, PTS1 PROTEIN-PEPTIDE COMPLEX, TETRATRICOPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT
1238	1fch	A	98	345	4.8e-29	0.46	1.00		PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: C, D;	SIGNALING PROTEIN PEROXISOMORE RECEPTOR 1, PTS1-BP, PEROXIN-5, PTS1 PROTEIN-PEPTIDE COMPLEX, TETRATRICOPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT
1241	1edh	A	34	152	3.2e-20	0.10	0.55		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
1241	1edh	A	52	253	6.8e-27	-0.19	0.76		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
1241	1edh	A	83	255	4.8e-17	0.21	0.64		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1

SEQ NO;	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
1241	1nc1	B	206	253	5.1e-06	-0.07	0.04		N-CADHERIN; INCI 3	CELL ADHESION PROTEIN
1241	1nc1	B	56	132	1.7e-05	0.15	0.31		N-CADHERIN; INCI 3	CADHERIN INCI 13
1241	1ncj	A	34	132	1.4e-21	-0.20	0.28		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN
1241	1ncj	A	43	253	1.7e-21	-0.03	0.65		N-CADHERIN; CHAIN: A;	ADHESION PROTEIN
1241	1ncj	A	90	255	6.4e-17	-0.20	0.35		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN
1241	1ncj	A	358	549	3.4e-20	-0.08	0.40		LAMININ ALPHA2 CHAIN; CHAIN: A, B, C, D;	ADHESION PROTEIN
										METAL BINDING PROTEIN BETA SANDWICH, CALCIUM-BINDING PROTEIN, METAL BINDING 2
1241	1suh		43	154	1.7e-07	-0.22	0.04		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOGULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
1246	1a5e		132	262	3.4e-30	0.56	1.00		TUMOR SUPPRESSOR P16INK4A; CHAIN: NULL;	ANTI-ONCOGENE CELL CYCLE, ANTI-ONCOGENE, REPEAT, ANK REPEAT
1246	1a5e		166	330	3.4e-30	0.40	1.00		TUMOR SUPPRESSOR P16INK4A; CHAIN: NULL;	ANTI-ONCOGENE CELL CYCLE, ANTI-ONCOGENE, REPEAT, ANK REPEAT
1246	1a5e		202	359	5.1e-29	0.84	1.00		TUMOR SUPPRESSOR P16INK4A; CHAIN: NULL;	ANTI-ONCOGENE CELL CYCLE, ANTI-ONCOGENE, REPEAT, ANK REPEAT
1246	1a5e		233	385	1.5e-29	0.39	0.93		TUMOR SUPPRESSOR P16INK4A; CHAIN: NULL;	ANTI-ONCOGENE CELL CYCLE, ANTI-ONCOGENE, REPEAT, ANK REPEAT
1246	1a5e		233	393	3.4e-30			66.97	TUMOR SUPPRESSOR	ANTI-ONCOGENE CELL CYCLE,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	FMF score	SEQFOL D score	Compound	PDB annotation
									P1GINK4A; CHAIN: NULL;	ANTI-ONCOGENE, REPEAT, ANK REPEAT
1246	lawc	B	145	298	1e-43	1.05	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1246	lawc	B	14	165	1e-39	0.93	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1246	lawc	B	150	298	9.6e-41	0.97	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1246	lawc	B	17	165	1.6e-38	0.93	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1246	lawe	B	183	332	3.4e-39	0.84	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA) DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1246	lawe	B	184	332	9.6e-35	0.55	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA) DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1246	lawe	B	212	362	1e-40	0.77	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA) DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1246	lawe	B	212	363	1e-43			90.97	GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA) DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1246	lawe	B	217	395	3.2e-32	0.21	0.23		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA;

SEQ ID NO:	PDB ID	CHAI ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	GABPBETAI; COMPLEX (TRANSCRIPTION REGULATION/DNA) DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1246	1awc	B	3	132	1.6e-33	0.88	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETAI; COMPLEX (TRANSCRIPTION REGULATION/DNA) DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1246	1awc	B	45	199	8.5e-39	0.55	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETAI; COMPLEX (TRANSCRIPTION REGULATION/DNA) DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1246	1awc	B	50	199	9.6e-37	0.68	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETAI; COMPLEX (TRANSCRIPTION REGULATION/DNA) DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1246	1bd8		145	301	8e-30			87.65	P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1246	1bd8		153	301	8e-30	0.58	1.00		P19INK4D CDK4/6 INHIBITOR;	TUMOR SUPPRESSOR TUMOR

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									CHAIN: NULL;	SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1246	1bi7	B	244	365	1.7e-28	0.57	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; MULTIPLE TUMOR SUPPRESSOR; CHAIN: B;	COMPLEX (KINASE/ANTI-ONCOGENE) CDK6; P19INK4A, MTS1; CYCLIN-DEPENDENT KINASE, CYCLIN-DEPENDENT KINASE INHIBITORY 2 PROTEIN, CDK, INK4, CELL CYCLE, MULTIPLE TUMOR SUPPRESSOR, 3 MTS1, COMPLEX (KINASE/ANTI-ONCOGENE) HEADER
1246	1bi6	B	114	304	3.4e-38	0.10	0.10		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1246	1bi6	B	13	170	1.7e-39	0.93	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1246	1bi6	B	147	303	6.8e-40			78.94	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1246	1bi6	B	183	338	3.4e-38	0.73	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX

SEQ NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fsi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1246	1bix	B	215	368	1.7e-38	0.89	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	(INHIBITOR PROTEIN/KINASE) COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1246	1bix	B	50	205	1.5e-38	0.70	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1246	1bix	B	82	237	6.8e-40	1.03	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1246	1bu9	A	144	310	6.8e-37	0.78	1.00		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
1246	1bu9	A	150	303	1.6e-36	0.97	1.00		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
1246	1bu9	A	17	170	9.6e-37	0.87	1.00		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1246	1bu9	A	181	338	1e-35	0.61	1.00		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C; TUMOR SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
1246	1bu9	A	184	367	8e-33	0.25	0.99		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C; TUMOR SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
1246	1bu9	A	215	373	3.4e-35	0.63	1.00		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C; TUMOR SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
1246	1bu9	A	243	394	6.8e-33	0.79	1.00		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C; TUMOR SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
1246	1bu9	A	3	174	3.4e-37	0.47	0.51		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C; TUMOR SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
1246	1bu9	A	44	205	1.7e-39	0.94	1.00		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C; TUMOR SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
1246	1bu9	A	9	177	1.7e-39			89.81	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C; TUMOR SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Binst	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1246	1lib	A	130	302	6.4e-36	0.88	1.00		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	HORMONE/GROWTH FACTOR CELL CYCLE INHIBITOR P18-INK4C(NK6); CELL CYCLE INHIBITOR, P18-INK4C(NK6); ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
1246	1lib	A	17	169	3.2e-36	0.78	1.00		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18-INK4C(NK6); CELL CYCLE INHIBITOR, P18-INK4C(NK6); ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
1246	1lib	A	184	366	3.2e-32	0.28	1.00		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18-INK4C(NK6); CELL CYCLE INHIBITOR, P18-INK4C(NK6); ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
1246	1lib	A	81	236	3.2e-36			83.68	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18-INK4C(NK6); CELL CYCLE INHIBITOR, P18-INK4C(NK6); ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
1246	1lan	D	12	186	4.8e-35	0.47	1.00		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65, P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
1246	1lan	D	179	346	1.6e-30	0.20	0.92		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65, P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
1246	1lan	D	212	404	1.6e-34	0.22	0.35		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65, P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
1246	1lan	D	45	232	8e-43	0.18	1.00		NF-KAPPA-B P65 SUBUNIT;	TRANSCRIPTION FACTOR P65;

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Fsi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1246	1inf	E	17	170	3.4e-38	0.85	1.00		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E; F ₁	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REG/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1246	1inf	E	210	404	9.6e-35	0.26	0.21		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E; F ₁	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REG/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1246	1inf	E	215	394	1.5e-44	0.53	1.00		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E; F ₁	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REG/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1246	1inf	E	43	238	1.7e-51	0.53	1.00		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E; F ₁	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REG/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1246	1inf	E	43	242	1.7e-51			89.07	NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E; F ₁	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REG/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1246	1inf	E	44	232	1.6e-42	0.74	1.00		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E; F ₁	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REG/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1246	1inf	E	82	278	5.1e-50	0.66	1.00		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E; F ₁	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REG/ANK REPEAT), ANKYRIN 2 REPEAT HELIX

SEQ ID NO:	PDB ID	CHAIN ID	STAR T.AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1246	1sw6	A	76	320	1.3e-21			60.99	REGULATORY PROTEIN SW16; CHAIN: A, B;	ANKYRIN 2 REPEAT HELIX TRANSCRIPTION REGULATION ANKYRIN REPEATS, CELL-CYCLE COMPLEX (ANTI- ONCOGENE/ANKYRIN REPEATS) P3BP2; ANKYRIN REPEATS, SH3, P53, TUMOR SUPPRESSOR, MULTIGENE 2 FAMILY, NUCLEAR PROTEIN, PHOSPHORYLATION, DISEASE MUTATION, 3 POLYMORPHISM, COMPLEX (ANTI- ONCOGENE/ANKYRIN REPEATS)
1246	1yes	B	214	398	3.2e-18			66.71	P53; CHAIN: A; 53BP2; CHAIN: B;	
1250	1eun	A	375	591	5.1e-12	-0.03	0.29		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 22 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1250	1eun	A	436	651	5.1e-07	0.02	0.03		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 22 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1250	1hae		120	150	0.0051	0.07	0.11		HERGULIN-ALPHA; CHAIN: NULL;	GROWTH FACTOR NEU DIFFERENTIATION FACTOR (RAT), ACETYLCHOLINE GROWTH FACTOR
1250	1hre		120	150	0.0051	0.13	0.25		GROWTH FACTOR HERGULIN-ALPHA (EPIDERMAL GROWTH FACTOR-LIKE DOMAIN) 1HRE 3 (NMR, MINIMIZED AVERAGE STRUCTURE) 1HRE 4	

SEQ NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1252	1d4v	A	326	426	5.1e-10	0.10	-0.14		TNF-RELATED APOPTOSIS INDUCING LIGAND: CHAIN: B; DEATH RECEPTOR 5; CHAIN: A;	APOPTOSIS TRAIL: DR5; LIGAND- RECEPTOR COMPLEX, TRIMERIC JELLY-ROLL, TNF-R 2 SUPERFAMILY; APOPTOSIS
1252	1dnn	L	351	449	8e-09	0.06	-0.13		BLOOD COAGULATION FACTOR VIIA; CHAIN: L; H; SOLUBLE TISSUE FACTOR; CHAIN: T; U: D-PHE-PHE-ARG- CHLOROMETHYLKETONE (DFRCMK) WITH CHAIN: C;	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)
1252	1dks	I	233	346	3.2e-12	0.02	-0.20		THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN HEAVY CHAIN; CHAIN: M, N; O, P; THROMBOMODULIN; CHAIN: I, J, K, L; THROMBIN INHIBITOR L-GLU-L-GLY-L- ARM; CHAIN: E, F, G, H;	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN, TM, CD141 ANTIGEN; EGR-CMK SERINE PROTEINASE, EGF-LIKE DOMAINS, ANTICOAGULANT COMPLEX, 2 ANTIFIBRINOLYTIC COMPLEX
1252	1dks	I	268	394	6.4e-15	0.03	-0.20		THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN HEAVY CHAIN; CHAIN: M, N; O, P; THROMBOMODULIN; CHAIN: I, J, K, L; THROMBIN INHIBITOR L-GLU-L-GLY-L- ARM; CHAIN: E, F, G, H;	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN, TM, CD141 ANTIGEN; EGR-CMK SERINE PROTEINASE, EGF-LIKE DOMAINS, ANTICOAGULANT COMPLEX, 2 ANTIFIBRINOLYTIC COMPLEX
1252	1dks	I	308	436	1.1e-12	0.10	-0.19		THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN HEAVY CHAIN; CHAIN: M, N; O, P; THROMBOMODULIN; CHAIN: I, J, K, L; THROMBIN INHIBITOR L-GLU-L-GLY-L- ARM; CHAIN: E, F, G, H;	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN, TM, CD141 ANTIGEN; EGR-CMK SERINE PROTEINASE, EGF-LIKE DOMAINS, ANTICOAGULANT COMPLEX, 2

SEQ NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1252	1enn		307	395	1.6e-13	0.24	0.04		FIBRILLIN; CHAIN: NULL;	ANTIFIBRINOLYTIC COMPLEX MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN; 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN
1252	1enn		351	431	3.2e-10	0.08	-0.19		FIBRILLIN; CHAIN: NULL;	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN; 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN
1252	1klo		225	419	8.5e-39	0.17	0.93		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
1252	1klo		234	411	8.5e-39			132.10	LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
1252	1klo		293	452	1.6e-20	0.40	0.51		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
1252	1klo		358	496	3.2e-18	-0.00	-0.03		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
1252	1prk	L	351	441	3.2e-09	0.10	-0.17		FACTOR IXA; CHAIN: C, L ₁ ; D; PHE-PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/VEGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM- BINDING, HYDROLASE, 3 GLYCOPROTEIN
1252	1slz		319	414	3.4e-17	0.34	-0.14		ANTISTASIN; CHAIN: NULL;	SERINE PROTEASE INHIBITOR FACTOR XA INHIBITOR; ANTISTASIN, CRYSTAL STRUCTURE, FACTOR XA INHIBITOR, 2 SERINE PROTEASE

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1252	1skz		355	425	5.1e-10	0.16	0.19		ANTISTASIN; CHAIN: NULL;	INHIBITOR, THROMBOSIS SERINE PROTEASE INHIBITOR FACTOR XA INHIBITOR; ANTISTASIN, CRYSTAL STRUCTURE, FACTOR XA INHIBITOR, 2 SERINE PROTEASE INHIBITOR, THROMBOSIS
1252	1kxa	L	355	448	3.2e-09	0.14	-0.18		BLOOD COAGULATION FACTOR XA; CHAIN: L; C;	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN
1252	4mt2		368	428	1.3e-09	-0.05	0.00		METALLOTHIONEIN METALLOTHIONEIN ISOFORM II.4MT2.3	
1252	9wga	A	298	492	4.8e-15	0.04	-0.19		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA.3	
1253	1one	A	11	134	9.6e-61	0.25	1.00		ENOLASE; CHAIN: A; B;	LYASE 2-PHOSPHO-D-GLYCERATE HYDROLASE; LYASE, GLYCOLYSIS
1253	1pdz		11	137	8e-63	0.15	1.00		ENOLASE; IPDZ 4 CHAIN: NULL; IPDZ 5	LYASE (CARBON-OXYGEN) 2- PHOSPHO-D-GLYCERATE DEHYDRATASE; IPDZ 6
1256	1kpf		53	163	9.6e-41	0.96	1.00		PROTEIN KINASE C INTERACTING PROTEIN; CHAIN: NULL;	PROTEIN KINASE INHIBITOR PKC- I, PROTEIN KINASE C INHIBITOR 1, HINT PROTEIN KINASE INHIBITOR, PKC-1, HIT PROTEIN FAMILY, 2 HISTIDINE TRIAD PROTEIN FAMILY, NUCLEOTIDYL HYDROLASE, 3 NUCLEOTIDYL TRANSFERASE
1256	1kpf		53	163	9.6e-41			144.01	PROTEIN KINASE C	PROTEIN KINASE INHIBITOR PKC-I

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fst Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									INTERACTING PROTEIN; CHAIN: NULL;	1. PROTEIN KINASE C INHIBITOR 1; HINT PROTEIN KINASE INHIBITOR, PKC δ 1, HIT PROTEIN FAMILY, 2 HISTIDINE TRIAD PROTEIN FAMILY; NUCLEOTIDYL HYDROLASE, 3 NUCLEOTIDYL TRANSFERASE
1256	4rhv		47	163	6.4e-41			147.29	HISTIDINE TRIAD NUCLEOTIDE-BINDING PROTEIN; CHAIN: NULL;	NUCLEOTIDE-BINDING PROTEIN HINT; NUCLEOTIDE-BINDING PROTEIN
1256	4rhv		52	163	6.4e-41	0.86	1.00		HISTIDINE TRIAD NUCLEOTIDE-BINDING PROTEIN; CHAIN: NULL;	NUCLEOTIDE-BINDING PROTEIN HINT; NUCLEOTIDE-BINDING PROTEIN
1257	1a5e		39	151	1.4e-21	0.27	0.48		TUMOR SUPPRESSOR P16INK4A; CHAIN: NULL;	ANTI-ONCOGENE CELL CYCLE, ANTI-ONCOGENE, REPEAT, ANK REPEAT
1257	1a5e		39	154	8e-26	0.80	1.00		TUMOR SUPPRESSOR P16INK4A; CHAIN: NULL;	ANTI-ONCOGENE CELL CYCLE, ANTI-ONCOGENE, REPEAT, ANK REPEAT
1257	1a5e		61	162	3.4e-25	0.65	1.00		TUMOR SUPPRESSOR P16INK4A; CHAIN: NULL;	ANTI-ONCOGENE CELL CYCLE, ANTI-ONCOGENE, REPEAT, ANK REPEAT
1257	1a5e		6	121	4.8e-18	0.16	0.40		TUMOR SUPPRESSOR P16INK4A; CHAIN: NULL;	ANTI-ONCOGENE CELL CYCLE, ANTI-ONCOGENE, REPEAT, ANK REPEAT
1257	1awe	B	39	164	6.4e-37	0.61	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA I; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABP ALPHA; GABP BETA I; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING; 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR

SEQ NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1257	1awc	B	4	154	9.6e-40	0.40	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D; E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA) DNA-BINDING; 2 NUCLEAR PROTEIN; ETS DOMAIN; ANKYRIN REPEATS; TRANSCRIPTION 3 FACTOR TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1257	1bd8		7	137	1.3e-31	0.48	1.00		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	COMPLEX (KINASE/ANTI-ONCOGENE) CDK6; P19INK4A; MTS1; CYCLIN DEPENDENT KINASE, CYCLIN DEPENDENT KINASE INHIBITORY 2 PROTEIN, CDK, INK4, CELL CYCLE, MULTIPLE TUMOR SUPPRESSOR, 3 MTS1, COMPLEX (KINASE/ANTI-ONCOGENE) HEADER
1257	1bt7	B	39	154	3.2e-26	0.62	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; MULTIPLE TUMOR SUPPRESSOR; CHAIN: B;	COMPLEX (KINASE/ANTI-ONCOGENE) CDK6; P19INK4A; MTS1; CYCLIN DEPENDENT KINASE, CYCLIN DEPENDENT KINASE INHIBITORY 2 PROTEIN, CDK, INK4, CELL CYCLE, MULTIPLE TUMOR SUPPRESSOR, 3 MTS1, COMPLEX (KINASE/ANTI-ONCOGENE) HEADER
1257	1bt7	B	6	121	8e-19	0.22	0.35		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; MULTIPLE TUMOR SUPPRESSOR; CHAIN: B;	COMPLEX (KINASE/ANTI-ONCOGENE) CDK6; P19INK4A; MTS1; CYCLIN DEPENDENT KINASE, CYCLIN DEPENDENT KINASE INHIBITORY 2 PROTEIN, CDK, INK4, CELL CYCLE, MULTIPLE TUMOR SUPPRESSOR, 3 MTS1, COMPLEX (KINASE/ANTI-ONCOGENE) HEADER
1257	1btx	B	39	164	1.7e-32	0.82	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verity score	PMF score	SEQFOL D score	Compound	PDB annotation
1257	1bk	B	7	157	1.6e-30	0.38	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	(INHIBITOR, PROTEIN/KINASE) COMPLEX (INHIBITOR, PROTEIN/KINASE) INHIBITOR, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR, PROTEIN/KINASE)
1257	1bu9	A	6	159	8e-37	0.34	0.88		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
1257	1d0s	A	39	154	1.6e-26	0.70	1.00		CYCLIN-DEPENDENT KINASE 4 INHIBITOR B; CHAIN: A;	SIGNALING PROTEIN HELIX-TURN-HELIX, ANKYRIN REPEAT
1257	1d0s	A	6	127	3.2e-20	0.42	0.95		CYCLIN-DEPENDENT KINASE 4 INHIBITOR B; CHAIN: A;	SIGNALING PROTEIN HELIX-TURN-HELIX, ANKYRIN REPEAT
1257	1dcq	A	2	91	6.4e-15	0.41	0.80		PTK2-ASSOCIATED PROTEIN BETA; CHAIN: A;	METAL BINDING PROTEIN ZINC-BINDING MODULE, ANKYRIN REPEATS, METAL BINDING PROTEIN
1257	1dcq	A	71	157	1.1e-17	0.05	0.99		PTK2-ASSOCIATED PROTEIN BETA; CHAIN: A;	METAL BINDING PROTEIN ZINC-BINDING MODULE, ANKYRIN REPEATS, METAL BINDING PROTEIN
1257	1lhb	A	6	158	4.8e-36	0.32	1.00		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18-INK4C/INK6; CELL CYCLE INHIBITOR, P18-INK4C/INK6, ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
1257	1lhb	A	73	163	8e-18	0.47	1.00		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18-INK4C/INK6; CELL CYCLE INHIBITOR, P18-INK4C/INK6, ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR

SEQ NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1257	1lin	D	4	162	8e-38	0.08	0.84		NE-KAPPA-B P65 SUBUNIT; CHAIN: A; NE-KAPPA-B P50D SUBUNIT; CHAIN: C; L-KAPPA-B-ALPHA; CHAIN: D; MYOTROPHIN; CHAIN: NULL	TRANSCRIPTION FACTOR P65; P50D: TRANSCRIPTION FACTOR, IKBNKB COMPLEX
1257	1myo		35	152	3.2e-26			32.27	MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT
1257	1myo		40	156	3.2e-26	0.32	0.98		MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT
1257	1myo		5	106	6.4e-24	0.22	0.98		MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT
1257	1myo		74	164	1.1e-23	0.04	1.00		MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT
1257	1nfi	E	4	162	1.6e-38	0.39	1.00		NE-KAPPA-B P65; CHAIN: A; C; NE-KAPPA-B P50; CHAIN: B; D; L-KAPPA-B-ALPHA; CHAIN: E; F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1257	1yes	B	12	95	1.4e-19	0.04	0.86		P53; CHAIN: A; 53BP2; CHAIN: B;	COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS) P53BP2; ANKYRIN REPEATS, SH3, P53, TUMOR SUPPRESSOR, MULTIGENE 2 FAMILY, NUCLEAR PROTEIN, PHOSPHORYLATION, DISEASE MUTATION, 3 POLYMORPHISM, COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS)
1257	1yes	B	39	154	1.6e-25	0.24	1.00		P53; CHAIN: A; 53BP2; CHAIN: B;	COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS) P53BP2; ANKYRIN REPEATS, SH3, P53, TUMOR SUPPRESSOR, MULTIGENE 2 FAMILY, NUCLEAR PROTEIN, PHOSPHORYLATION, DISEASE MUTATION, 3 POLYMORPHISM, COMPLEX (ANTI-

SEQ ID NO:	PDB ID	CHAI ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1257	1yes	B	73	161	1.6e-22	0.44	1.00		P53; CHAIN: A; 5BP2; CHAIN: B;	ONCOGENE/ANKYRIN REPEATS) COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS) P53BP2, ANKYRIN REPEATS, SH3, P53, TUMOR SUPPRESSOR, MULTIGENE 2 FAMILY, NUCLEAR PROTEIN, PHOSPHORYLATION, DISEASE MUTATION, 3 POLYMORPHISM, COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS)
1258	1arf	1	3	183	3.4e-20			52.08	MANNANOSE-BINDING PROTEIN-A; IAFB 4 CHAIN: 1, 2, 3; IAFB 5	LECTIN GL-QPDWG; IAFB 7 C-TYPE LECTIN, CALCIUM-BINDING PROTEIN IAFB 22
1258	1b3	A	31	180	8e-34	0.42	0.11		COAGULATION FACTOR IX-BINDING PROTEIN A; CHAIN: A; COAGULATION FACTOR IX-BINDING PROTEIN B; CHAIN: B;	COLLAGEN BINDING PROTEIN IX-BP; IX-BP; COAGULATION FACTOR IX-BINDING, HETERODIMER, VENOM, HABU 2 SNAKE, C-TYPE LECTIN SUPERFAMILY, COLLAGEN BINDING PROTEIN
1258	1b3	A	34	181	8e-34			61.48	COAGULATION FACTOR IX-BINDING PROTEIN A; CHAIN: A; COAGULATION FACTOR IX-BINDING PROTEIN B; CHAIN: B;	COLLAGEN BINDING PROTEIN IX-BP; IX-BP; COAGULATION FACTOR IX-BINDING, HETERODIMER, VENOM, HABU 2 SNAKE, C-TYPE LECTIN SUPERFAMILY, COLLAGEN BINDING PROTEIN
1258	1c3a	A	31	185	6.4e-28	0.20	0.80		FLAVOCETIN-A: ALPHA SUBUNIT; CHAIN: A; FLAVOCETIN-A: BETA SUBUNIT; CHAIN: B	MEMBRANE PROTEIN C-TYPE LECTIN-LIKE DOMAINS
1258	1c3a	B	31	183	1.4e-30	0.03	0.01		FLAVOCETIN-A: ALPHA SUBUNIT; CHAIN: A; FLAVOCETIN-A: BETA SUBUNIT; CHAIN: B	MEMBRANE PROTEIN C-TYPE LECTIN-LIKE DOMAINS

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fst Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1258	1dvh	A	31	180	6.4e-28	0.72	0.68		ASIALOGLYCOPROTEIN RECEPTOR 1; CHAIN: A;	SIGNALING PROTEIN HEPATIC LECTIN HI; C-TYPE LECTIN CRD
1258	1esn	I	52	80	0.0093	-0.69	0.57		INTIMIN; CHAIN: I;	INTIMIN INT19; INTIMIN, ESCHERICHIA COLI, CELL ADHESION, OUTER MEMBRANE 2 PROTEIN, NMR SPECTROSCOPY
1258	1egg	B	29	187	1.6e-29	0.41	0.36		MACROPHAGE MANNOSE RECEPTOR; CHAIN: A, B;	SUGAR BINDING PROTEIN C-TYPE LECTIN, MANNOSE RECEPTOR
1258	1esl		44	213	4.8e-30	0.45	0.89		CELL ADHESION PROTEIN E-SELECTIN (LECTIN AND EGF DOMAINS, RESIDUES 1 - 157) IESL 3 (FORMERLY KNOWN AS ELAM-1) IESL 4	
1258	1esl		45	220	4.8e-30			60.26	CELL ADHESION PROTEIN E-SELECTIN (LECTIN AND EGF DOMAINS, RESIDUES 1 - 157) IESL 3 (FORMERLY KNOWN AS ELAM-1) IESL 4	
1258	1f00	I	52	80	0.0093	-0.19	0.40		INTIMIN; CHAIN: I;	CELL ADHESION IMMUNOGLOBULIN-LIKE FOLD, C-TYPE LECTIN-LIKE FOLD
1258	1hnn		12	184	1.3e-23			68.61	TETRANECTIN; CHAIN: NULL;	LECTIN TETRANECTIN, PLASMINOGEN BINDING, KRINGLE 4, ALPHA-HELICAL 2 COILED COIL, C-TYPE LECTIN, CARBOHYDRATE RECOGNITION DOMAIN
1258	1hnp		8	183	6.4e-21			50.48	MANNOSE-BINDING PROTEIN; IHUP 4 CHAIN: NULL; IHUP 5	C-TYPE LECTIN ALPHA-HELICAL COILED-COIL IHUP 12
1258	1lxx	A	31	180	4.8e-32	0.21	0.21		COAGULATION FACTORS IXA-BP COAGULATION FACTOR IXA-BINDING PROTEIN; CHAIN: A, B, C, D, E, F;	COAGULATION FACTOR BINDING IXA-BP COAGULATION FACTOR BINDING, C-TYPE LECTIN, GLA-DOMAIN 2 BINDING, C-TYPE CRD MOTIF, LOOP EXCHANGED DIMER
1258	1lxx	A	34	181	4.8e-32			36.55	COAGULATION FACTORS	COAGULATION FACTOR BINDING

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	FMF score	SEQFOL D score	Counpound	PDB annotation
									IXA-BINDING PROTEIN; CHAIN: A, B, C, D, E, F;	IXA-BP COAGULATION FACTOR BINDING, C-TYPE LECTIN, GLA-DOMAIN 2 BINDING, C-TYPE CRD MOTIF, LOOP EXCHANGED DIMER
1258	1lxx	B	31	183	1.3e-29	0.24	0.45		COAGULATION FACTORS IXA-BP COAGULATION FACTOR BINDING, C-TYPE LECTIN, GLA-DOMAIN 2 BINDING, C-TYPE CRD MOTIF, LOOP EXCHANGED DIMER	COAGULATION FACTOR BINDING IXA-BP COAGULATION FACTOR BINDING, C-TYPE LECTIN, GLA-DOMAIN 2 BINDING, C-TYPE CRD MOTIF, LOOP EXCHANGED DIMER
1258	1lxx	B	34	183	1.3e-29			53.06	COAGULATION FACTORS IXA-BINDING PROTEIN; CHAIN: A, B, C, D, E, F;	COAGULATION FACTOR BINDING IXA-BP COAGULATION FACTOR BINDING, C-TYPE LECTIN, GLA-DOMAIN 2 BINDING, C-TYPE CRD MOTIF, LOOP EXCHANGED DIMER
1258	1lit		31	182	1.6e-31	0.51	0.30		LITHOSTATHINE; CHAIN: NULL	PANCREATIC STONE INHIBITOR PANCREATIC STONE INHIBITOR, LECTIN
1258	1lit		31	183	1.6e-31			71.84	LITHOSTATHINE; CHAIN: NULL	PANCREATIC STONE INHIBITOR PANCREATIC STONE INHIBITOR, LECTIN
1258	1qdd	A	18	183	1.6e-31			72.35	LITHOSTATHINE; CHAIN: A;	METAL BINDING PROTEIN PANCREATIC STONE PROTEIN, PSP; PANCREATIC STONE INHIBITOR, LITHOSTATHINE
1258	1qdd	A	31	182	1.6e-31	0.65	0.52		LITHOSTATHINE; CHAIN: A;	METAL BINDING PROTEIN PANCREATIC STONE PROTEIN, PSP; PANCREATIC STONE INHIBITOR, LITHOSTATHINE
1258	1tm	1	3	183	5.1e-19			50.72	LECTIN MANNOSE-BINDING PROTEIN A (CLOSTRIDIUM FRAGMENT) (CL-MBP-A) IRTM 3 IRTM 96	
1258	1tm3		28	184	1.2e-24			59.80	TETRAPECTIN; CHAIN: NULL;	LECTIN TETRAPECTIN, PLASMINOGEN BINDING, KRINGLE

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	F ₅₀ Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									4. C-TYPE LECTIN, 2 CARBOHYDRATE RECOGNITION DOMAIN	
1258	2ulp	A	29	179	1.6e-27	-0.06	0.51		SEA RAVEN TYPE II ANTIFREEZE PROTEIN; CHAIN: A;	ANTIFREEZE PROTEIN RECOMBINANT SEA RAVEN PROTEIN, SOLUTION BACKBONE FOLD, C-2 TYPE LECTIN, ANTIFREEZE PROTEIN
1259	1dap	A	1	33	4.8e-05	-0.51	0.13		DIAMINOPTIMELIC ACID DEHYDROGENASE; CHAIN: A; B;	OXIDOREDUCTASE DAPDH; NADP+ DEHYDROGENASE, D-AMINO ACID DEHYDROGENASE, LYSINE 2 BIOSYNTHESIS, ASYMMETRIC DIMER, OXIDOREDUCTASE
1259	3gpd	R	2	336	0			491.59	OXIDOREDUCTASE (NAD(S)-ALDEHYDE(D)) D-GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE (EC.1.2.1.12) 3GPD 4	
1259	3gpd	R	3	336	0	0.93	1.00		OXIDOREDUCTASE (NAD(S)-ALDEHYDE(D)) D-GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE (EC.1.2.1.12) 3GPD 4	
1263	1a7c	A	82	463	4.8e-91			115.78	PLASMINOGEN ACTIVATOR INHIBITOR TYPE 1; CHAIN: A; PENTAPEPTIDE; CHAIN: B; C	COMPLEX (PROTEASE INHIBITOR(PEPTIDE) PAI-1; SERINE PROTEASE INHIBITOR, PAI-1, CARBOHYDRATE, INHIBITOR 2 COMPLEX, PEPTIDE SERPIN ACT; SERPIN, SERINE PROTEASE INHIBITOR,
1263	1as4	A	88	430	0	0.25	0.96		ANTICHTHMYOTRYPIN; CHAIN: A; B;	

SEQ NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQOL D score	Compound	PDB annotation
1263	1as4	A	50	438	0			104.85	ANTICHTYMOTRYPSIN; CHAIN: A, B;	ANTICHTYMOTRYPSIN SERPIN ACT; SERPIN, SERINE PROTEASE INHIBITOR, ANTICHTYMOTRYPSIN
1263	1ath	B	101	464	1.3e-96			102.92	HUMAN ANTI THROMBIN-III ANTI THROMBIN III IATH 3	
1263	1ath	B	85	464	1.3e-96	0.23	1.00		HUMAN ANTI THROMBIN-III ANTI THROMBIN III IATH 3	
1263	1by7	A	86	463	0	0.68	1.00		PLASMINOGEN ACTIVATOR INHIBITOR-2; CHAIN: A;	PROTEIN BINDING PAL-2; SERPIN, PROTEIN BINDING
1263	1by7	A	86	463	0			101.02	PLASMINOGEN ACTIVATOR INHIBITOR-2; CHAIN: A;	PROTEIN BINDING PAL-2; SERPIN, PROTEIN BINDING
1263	1d5s	B	433	463	1.3e-09	-0.75	0.04		PI-ARG ANTI TRYPSIN; CHAIN: A; PI-ARG ANTI TRYPSIN; CHAIN: B;	HYDROLASE; INHIBITOR SERPIN FOLD, RCI CLEAVAGE; A BETA SHEET POLYMERIZATION
1263	1db2	A	83	463	3.2e-94			120.11	PLASMINOGEN ACTIVATOR INHIBITOR-1; CHAIN: A, B;	HYDROLASE INHIBITOR NATIVE SERPIN, HYDROLASE INHIBITOR
1263	1ezx	A	86	432	0	0.23	0.80		ALPHA-1-ANTI TRYPSIN; CHAIN: A; ALPHA-1- ANTI TRYPSIN; CHAIN: B; TRYPSIN; CHAIN: C;	HYDROLASE/HYDROLASE INHIBITOR PROTEASE-INHIBITOR COMPLEX, SERPIN, ALPHA-1- ANTI TRYPSIN, 2 TRYPSIN
1263	1hle	A	85	426	3.2e-98	0.38	1.00		HYDROLASE INHIBITOR(SERINE PROTEINASE) HORSE LEUKOCYTE ELASTASE INHIBITOR (HLEI) HLE 3	
1263	1hle	A	85	432	3.2e-98			84.90	HYDROLASE INHIBITOR(SERINE PROTEINASE) HORSE LEUKOCYTE ELASTASE INHIBITOR (HLEI) HLE 3	
1263	1ova	A	80	463	0			126.84	SERPIN OVALBUMIN (EGG ALBUMIN) IOVA 3	
1263	1ova	A	87	463	0	0.62	1.00		SERPIN OVALBUMIN (EGG ALBUMIN) IOVA 3	

SEQ NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verity score	PMF score	SEQFOL D score	Compound	PDB annotation
1263	1qlp	A	86	463	0	0.49	1.00		ALBUMIN IIOVA 3 ALPHA-1-ANTITRYPSIN; CHAIN: A;	SERINE PROTEASE INHIBITOR, ALPHA-1-PROTEINASE INHIBITOR, ALPHA-1-ANTIPROTEINASE; SERINE PROTEASE INHIBITOR, SERPIN, GLYCOPROTEIN, SIGNAL, 2 POLYMORPHISM, EMPHYSEMA, DISEASE MUTATION, ACUTE PHASE
1263	1qlp	A	88	466	0			146.76	ALPHA-1-ANTITRYPSIN; CHAIN: A;	SERINE PROTEASE INHIBITOR ALPHA-1-PROTEINASE INHIBITOR, ALPHA-1-ANTIPROTEINASE; SERINE PROTEASE INHIBITOR, SERPIN, GLYCOPROTEIN, SIGNAL, 2 POLYMORPHISM, EMPHYSEMA, DISEASE MUTATION, ACUTE PHASE
1263	1qmb	B	433	463	4.8e-09	-0.75	0.12		ALPHA-1-ANTITRYPSIN; CHAIN: A, B;	SERINE PROTEASE INHIBITOR ALPHA-1-PROTEINASE INHIBITOR, ALPHA-1-PI; SERPIN, ANITRYPSIN, POLYMER, CLEAVED
1263	1qma	A	88	464	0	0.44	1.00		ALPHA-1- ANTITRYPSIN; CHAIN: A;	SERPIN AACT SERPIN, SERINE PROTEINASE INHIBITOR, PARTIAL LOOP 2 INSERTION, LOOP-SHEET POLYMERIZATION, EMPHYSEMA, DISEASE 3 MUTATION, ACUTE PHASE PROTEIN, CONFORMATIONAL DISEASE
1263	1esk		80	463	3.2e-85			102.05	SERPIN K; CHAIN: NULL;	SERINE PROTEASE INHIBITOR SERINE PROTEASE INHIBITOR, SERPIN, PROTEASE
1263	2ant	I	47	466	0			139.88	ANTITHROMBIN; CHAIN: L, I;	SERPIN SERPIN, HEPARIN, INHIBITOR
1263	2ant	I	49	464	0	0.48	1.00		ANTITHROMBIN; CHAIN: L, I;	SERPIN SERPIN, HEPARIN,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fsi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1263	2ant	L	59	466	0			125.53	ANTITHROMBIN; CHAIN: L; I;	INHIBITOR
1263	2ant	L	81	464	0	0.63	1.00		ANTITHROMBIN; CHAIN: L; I;	SERPIN SERPIN, HEPARIN, INHIBITOR
1264	1aln	A	25	218	6.4e-92	0.93	1.00		B*3501; CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C;	SERPIN SERPIN, HEPARIN, INHIBITOR
1264	1aln	A	25	219	1.2e-93			237.20	B*3501; CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C;	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)
1264	1aln	A	26	210	1.2e-93	1.19	1.00		B*3501; CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C;	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)
1264	1agd	A	25	218	3.2e-92	0.97	1.00		B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKKYKL - INDEX PEPTIDE); CHAIN: C;	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX
1264	1agd	A	25	219	3.2e-92			239.77	B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKKYKL - INDEX PEPTIDE); CHAIN: C;	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX
1264	1agd	A	26	210	8.5e-92	0.98	1.00		B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1264	1duz	A	25	218	1.6e-88	1.03	1.00		(GGKKK YKG - INDEX PEPTIDE); CHAIN: C; HLA-A*0201; CHAIN: A, D; BETA-2 MICROGLOBULIN; CHAIN: B; E; HTLV-1 OCTAMERIC TAX PEPTIDE; CHAIN: C, F;	HISTOCOMPATIBILITY COMPLEX
1264	1efk	A	25	218	9.6e-91	1.13	1.00		HLA-CW3 (HEAVY CHAIN); CHAIN: A; BETA-2- MICROGLOBULIN; CHAIN: B; PEPTIDE FROM IMPORTIN ALPHA-2; CHAIN: C; NATURAL KILLER CELL RECEPTOR KIR2DL2; CHAIN: D, E;	IMMUNE SYSTEM MHC, HLA, CLASS I, KIR, NK CELL RECEPTOR, IMMUNOGLOBULIN 2 FOLD, RECEPTOR/MHC COMPLEX
1264	1efk	A	26	210	8.5e-93	1.29	1.00		HLA-CW3 (HEAVY CHAIN); CHAIN: A; BETA-2- MICROGLOBULIN; CHAIN: B; PEPTIDE FROM IMPORTIN ALPHA-2; CHAIN: C; NATURAL KILLER CELL RECEPTOR KIR2DL2; CHAIN: D, E;	IMMUNE SYSTEM MHC, HLA, CLASS I, KIR, NK CELL RECEPTOR, IMMUNOGLOBULIN 2 FOLD, RECEPTOR/MHC COMPLEX
1264	1hoc	A	25	218	1.6e-84			206.63	HISTOCOMPATIBILITY ANTIGEN MURINE CLASS I MAJOR HISTOCOMPATIBILITY COMPLEX CONSISTING 1HOC 3 OF H-2D-B* B2- MICROGLOBULIN, AND A 9- RESIDUE PEPTIDE 1HOC 4	
1264	1hsa	A	25	218	3.2e-91	0.91	1.00		HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN 1HSA 3/HLA- B*ASTERSKJ27055 1HSA 4	
1264	1hsa	A	25	219	3.2e-91			231.27	HISTOCOMPATIBILITY	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fsi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN I HSA 3 /HLA-B*AS*TERLSE2703\$ I HSA 4	
1264	1hsb	A	25	218	3.2e-89	1.15	1.00		HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN AW68.1 (LEUCOCYTE I HSB 3 ANTIGEN) I HSB 4	
1264	1hsb	A	25	219	3.2e-89			226.78	HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN AW68.1 (LEUCOCYTE I HSB 3 ANTIGEN) I HSB 4	
1264	1mhe	A	26	219	4.8e-88			209.47	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-E; CHAIN: A, C; BETA-2-MICROGLOBULIN; CHAIN: B, D; PEPTIDE (VMAPRTVLL); CHAIN: P, Q;	MAJOR HISTOCOMPATIBILITY COMPLEX MHC NONCLASSICAL CHAIN, MHC-E, HLA-E, MHC CLASS HLA-E, HLA E, MAJOR HISTOCOMPATIBILITY COMPLEX, MHC, HLA, 2 BETA 2 MICROGLOBULIN, PEPTIDE, LEADER PEPTIDE, 3 NON-CLASSICAL MHC, CLASS IB MHC IMMUNE SYSTEM
1264	1qpd	A	26	218	6.4e-89	1.17	1.00		HISTOCOMPATIBILITY LEUCOCYTE ANTIGEN (HLA)-CW4 CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HLA-CW4 SPECIFIC PEPTIDE; CHAIN: C;	IMMUNOGLOBULIN (IG)-LIKE DOMAIN, ALPHA HELIX, BETA SHEET, 2 IMMUNE SYSTEM
1264	1unc	A	25	199	9.6e-81			257.75	HISTOCOMPATIBILITY ANTIGEN TRUNCATED HUMAN CLASS I	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fsi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									HISTOCOMPATIBILITY ANTIGEN HLA-AW68 ITMC 3 COMPLEXED WITH A DECA-MERIC PEPTIDE (EVAPPEYHRK) ITMC 4	
1265	1aln	A	25	212	0	0.82	1.00		B*3501; CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C;	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)
1265	1aln	A	25	213	0			222.84	B*3501; CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C;	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)
1265	1agd	A	25	212	0	0.93	1.00		B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKKYKL - INDEX PEPTIDE); CHAIN: C;	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX
1265	1agd	A	25	213	0			242.14	B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKKYKL - INDEX PEPTIDE); CHAIN: C;	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX
1265	1efk	A	25	212	4.8e-100	0.96	1.00		HLA-CW3 (HEAVY CHAIN); CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; PEPTIDE FROM IMPORTIN ALPHA-2; CHAIN: C; NATURAL KILLER CELL RECEPTOR KIR2DL2; CHAIN: D, E;	IMMUNE SYSTEM MHC, HLA CLASS I, KIR, NK CELL RECEPTOR, IMMUNOGLOBULIN 2 FOLD, RECEPTOR/MHC COMPLEX
1265	1hsa	A	25	212	1.6e-100	1.04	1.00		HISTOCOMPATIBILITY	HISTOCOMPATIBILITY

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1265	1hsa	A	25	213	1.6e-100			212.48	ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY 'ANTIGEN IHS A 3 /HLA-B*(ASTERISK)2705\$ IHS A 4	
1265	1qpd	A	26	212	1.3e-98	0.83	1.00		ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN IHS A 3 /HLA-B*ASTERISK2705\$ IHS A 4	IMMUNE SYSTEM
1265	1tmc	A	25	199	3.2e-93	1.00	1.00		HISTOCOMPATIBILITY ANTIGEN TRUNCATED HUMAN CLASS I ANTIGEN HLA-A*W68 ITMC 3 COMPLEXED WITH A DECAMERIC PEPTIDE (EVAPEYHRK) ITMC 4	IMMUNOGLOBULIN (IG)-LIKE DOMAIN, ALPHA HELIX, BETA SHEET, 2 IMMUNE SYSTEM CHAIN: C;
1265	1tmc	A	25	199	3.2e-93			245.23	HISTOCOMPATIBILITY ANTIGEN TRUNCATED HUMAN CLASS I ANTIGEN HLA-A*W68 ITMC 3 COMPLEXED WITH A DECAMERIC PEPTIDE (EVAPEYHRK) ITMC 4	
1266	1a1n	A	22	210	4.8e-97	0.83	1.00		B*3501; CHAIN: A; B: PEPTIDE VP1RPMY; CHAIN: C;	COMPLEX (ANTIGEN/PEPTIDE) B3;5; MAJOR HISTOCOMPATIBILITY

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	FsI Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)
1266	1aln	A	22	210	4.3e-97			202.13	B*3501; CHAIN: A, B; PEPTIDE VPLRPMY; CHAIN: C;	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)
1266	1agd	A	22	210	1.1e-97	0.92	1.00		B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKKYKL - INDEX PEPTIDE); CHAIN: C;	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX (ANTIGEN/PEPTIDE)
1266	1agd	A	22	210	1.1e-97			212.14	B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKKYKL - INDEX PEPTIDE); CHAIN: C;	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX (ANTIGEN/PEPTIDE)
1266	1duz	A	22	208	4.8e-95	0.88	1.00		HLA-A*0201; CHAIN: A, D; BETA-2 MICROGLOBULIN; CHAIN: B; E; HTLV-1 OCTAMERIC TAX PEPTIDE; CHAIN: C, F;	IMMUNE SYSTEM IMMUNOGLOBULIN FOLD
1266	1efk	A	22	210	3.2e-96	1.08	1.00		HLA-CW3 (HEAVY CHAIN); CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; PEPTIDE FROM IMPORTIN ALPHA-2; CHAIN: C; NATURAL KILLER CELL RECEPTOR KIR2DL2; CHAIN: D, E;	IMMUNE SYSTEM MHC, HLA, CLASS I, KIR, NK CELL RECEPTOR, IMMUNOGLOBULIN 2 FOLD, RECEPTOR/MHC COMPLEX
1266	1hsa	A	22	210	3.2e-96	0.89	1.00		HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN IHS3 3/HLA-	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T.AA	END AA	FsI Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1266	1hsa	A	22	210	3.2e-96			195.27	B(ASTERISK)27055 IHS A 4 HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN IHS A 3 /HLA- B(ASTERISK)27055 IHS A 4	
1266	1hsb	A	22	208	4.8e-96	0.87	1.00		HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN AW68.1 (LEUCOCYTE IHSB 3 ANTIGEN) IHSB 4	
1266	1hsb	A	22	210	4.8e-96			189.34	HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN AW68.1 (LEUCOCYTE IHSB 3 ANTIGEN) IHSB 4	
1266	1qpd	A	23	210	3.2e-94	0.89	1.00		HISTOCOMPATIBILITY LEUCOCYTE ANTIGEN (HLA)- CW4 CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HLA-CW4 SPECIFIC PEPTIDE; CHAIN: C;	IMMUNE SYSTEM IMMUNOGLOBULIN (IG)-LIKE DOMAIN, ALPHA HELIX, BETA SHEET, 2 IMMUNE SYSTEM
1266	1tmc	A	22	197	4.8e-90	0.98	1.00		HISTOCOMPATIBILITY ANTIGEN TRUNCATED HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-AW68 I TMC 3 COMPLEXED WITH A DECAMERIC PEPTIDE (EVAPPEYHRK) I TMC 4	
1266	1tmc	A	22	197	4.8e-90			228.77	HISTOCOMPATIBILITY ANTIGEN TRUNCATED	

SEQ NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-A*68 ITMC 3 COMPLEXED WITH A DECA-MERIC PEPTIDE (EVAPETHRK) ITMC 4	
1267	1ain	A	25	214	6.4e-100	1.01	1.00		B*3501; CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C;	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NPF, COMPLEX (ANTIGEN/PEPTIDE)
1267	1ain	A	25	214	6.4e-100			206.29	B*3501; CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C;	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NPF, COMPLEX (ANTIGEN/PEPTIDE)
1267	1agd	A	25	214	1.6e-100	0.95	1.00		B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKKYKL - INDEX PEPTIDE); CHAIN: C;	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX
1267	1agd	A	25	214	1.6e-100			193.54	B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKKYKL - INDEX PEPTIDE); CHAIN: C;	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX
1267	1duz	A	25	214	3.2e-97	0.96	1.00		HLA-A*0201; CHAIN: A, D; BETA-2 MICROGLOBULIN; CHAIN: B; E; HTLV-1 OCTAMERIC TAX PEPTIDE; CHAIN: C, F;	IMMUNE SYSTEM IMMUNOGLOBULIN FOLD
1267	1etx	A	25	214	1.6e-98	0.91	1.00		HLA-CW3 (HEAVY CHAIN); CHAIN: A; BETA-2-	IMMUNE SYSTEM MHC, HLA, CLASS I, KIR, NK CELL RECEPTOR,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fsi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									MICROGLOBULIN; CHAIN: B; PEPTIDE FROM IMPORTIN ALPHA-2; CHAIN: C: NATURAL KILLER CELL RECEPTOR KIR2DL2; CHAIN: D: E;	IMMUNOGLOBULIN 2 FOLD, RECEPTOR/MHC COMPLEX
1267	1hsa	A	25	214	1.6e-99	1.02	1.00		HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN IHSB 3 /HLA-B*(ASERISK)27055 IHSB 4	
1267	1hsa	A	25	214	1.6e-99			198.64	HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN IHSB 3 /HLA-B*(ASERISK)27055 IHSB 4	
1267	1hsb	A	25	214	1.1e-98	0.98	1.00		HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN AW68.1 (LEUCOCYTE IHSB 3 (ANTIGEN) IHSB 4	
1267	1hsb	A	25	214	1.1e-98			190.28	HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN AW68.1 (LEUCOCYTE IHSB 3 (ANTIGEN) IHSB 4	
1267	1lqd	A	26	214	4.8e-97	0.95	1.00		HISTOCOMPATIBILITY LEUCOCYTE ANTIGEN (HLA)-CW4 CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HLA-CW4 SPECIFIC PEPTIDE; CHAIN: C;	IMMUNE SYSTEM IMMUNOGLOBULIN (IG)-LIKE DOMAIN, ALPHA HELIX, BETA SHEET, 2 IMMUNE SYSTEM
1267	1lme	A	25	200	6.4e-91	0.91	1.00		HISTOCOMPATIBILITY	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									ANTIGEN TRUNCATED HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-A*68 ITMC 3 COMPLEXED WITH A DECAMERIC PEPTIDE (EVAPPEYHRK) ITMC 4	
1267	1tmc	A	25	200	6.4e-91			227.42	HISTOCOMPATIBILITY ANTIGEN TRUNCATED HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-A*68 ITMC 3 COMPLEXED WITH A DECAMERIC PEPTIDE (EVAPPEYHRK) ITMC 4	
1268	1aln	A	25	301	0	0.83	1.00		B*3501: CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C;	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B*3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)
1268	1aln	A	25	301	0			381.69	B*3501: CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C;	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B*3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)
1268	1agd	A	25	301	0	0.79	1.00		B*0801: CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKKYKL - INDEX PEPTIDE); CHAIN: C;	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I HISTOCOMPATIBILITY COMPLEX
1268	1agd	A	25	301	0			382.18	B*0801: CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1268	1dn2	A	224	314	0.00034	-0.28	0.00		(GGKKYKL - INDEX PEPTIDE); CHAIN: C; IMMUNOGLOBULIN LAMBDA HEAVY CHAIN; CHAIN: A, B; ENGINEERED PEPTIDE; CHAIN: E, F;	HISTOCOMPATIBILITY COMPLEX
1268	1dnz	A	25	300	0	0.83	1.00		HLA-A*0201; CHAIN: A, D; BETA-2 MICROGLOBULIN; CHAIN: B, E; HTLV-1 OCTAMERIC TAX PEPTIDE; CHAIN: C, F;	IMMUNE SYSTEM IMMUNOGLOBULIN FOLD
1268	1efx	A	25	303	0	0.83	1.00		HLA-CW3 (HEAVY CHAIN); CHAIN: A; BETA-2-MICROGLOBULIN; CHAIN: B; PEPTIDE FROM IMPORTIN ALPHA-2; CHAIN: C; NATURAL KILLER CELL RECEPTOR KIR2DL2; CHAIN: D, E;	IMMUNE SYSTEM MHC, HLA, CLASS I, KIR, NK CELL RECEPTOR, IMMUNOGLOBULIN 2 FOLD, RECEPTOR/MHC COMPLEX
1268	1hsa	A	25	301	0	0.80	1.00		HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN I HSA 3 /HLA-B*ASTERISK27055 I HSA 4	
1268	1hsa	A	25	301	0			381.68	HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN I HSA 3 /HLA-B*ASTERISK27055 I HSA 4	
1268	1hsb	A	25	295	0	0.82	1.00		HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN A W68.1 (LEUCOCYTE I HSB 3 ANTIGEN) I HSB 4	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Ps Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1268	1hab	A	25	295	0			416.11	HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN AW68.1 (LEUCOCYTE IHSB 3 ANTIGEN) IHSB 4	
1268	1igt	B	224	308	1.6e-05	0.26	0.71		IGG2A INTACT ANTIBODY - MAB231; CHAIN: A, B, C, D	IMMUNOGLOBULIN INTACT IMMUNOGLOBULIN V REGION C REGION, IMMUNOGLOBULIN
1268	1mco	H	189	310	1.7e-05	0.09	0.23		IMMUNOGLOBULIN IMMUNOGLOBULIN G1 (IGG1) (MCG) WITH A HINGE DELETION IMCO 3	
1268	1mco	H	220	314	6.8e-06	0.30	0.48		IMMUNOGLOBULIN IMMUNOGLOBULIN G1 (IGG1) (MCG) WITH A HINGE DELETION IMCO 3	
1268	1ogd	A	26	299	0	0.63	1.00		HISTOCOMPATIBILITY LEUCOCYTE ANTIGEN (HLA)-CW4 CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HLA-CW4 SPECIFIC PEPTIDE; CHAIN: C;	IMMUNE SYSTEM IMMUNOGLOBULIN (IG)-LIKE DOMAIN, ALPHA HELIX, BETA SHEET, 2 IMMUNE SYSTEM
1269	1aln	A	25	285	0	0.88	1.00		B*3501; CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C;	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NBF, COMPLEX (ANTIGEN/PEPTIDE)
1269	1aln	A	25	288	0			279.39	B*3501; CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C;	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NBF, COMPLEX (ANTIGEN/PEPTIDE)

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1269	1agd	A	25	285	0	0.87	1.00		B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKKYKL - INDEX PEPTIDE); CHAIN: C;	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX
1269	1agd	A	25	288	0			278.31	B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKKYKL - INDEX PEPTIDE); CHAIN: C;	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX
1269	1duz	A	25	285	0	0.93	1.00		HLA-A*0201; CHAIN: A, D; BETA-2 MICROGLOBULIN; CHAIN: B; E; HTLV-1 OCTAMERIC TAX PEPTIDE; CHAIN: C, F;	IMMUNE SYSTEM IMMUNOGLOBULIN FOLD
1269	1e1x	A	25	285	0	0.94	1.00		HLA-CW3 (HEAVY CHAIN); CHAIN: A; BETA-2, MICROGLOBULIN; CHAIN: B; PEPTIDE FROM IMPORTIN ALPHA-2; CHAIN: C; NATURAL KILLER CELL RECEPTOR KIR2DL2; CHAIN: D, E;	IMMUNE SYSTEM MHC, HLA, CLASS I, KIR, NK CELL RECEPTOR, IMMUNOGLOBULIN 2 FOLD, RECEPTOR/MHC COMPLEX
1269	1hsa	A	25	285	0	0.93	1.00		HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN I HSA 3 /HLA- B(ASTERISK)2705\$ I HSA 4	
1269	1hsa	A	25	288	0			284.65	HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN I HSA 3 /HLA- B(ASTERISK)2705\$ I HSA 4	
1269	1hsb	A	25	285	0	0.93	1.00		HISTOCOMPATIBILITY ANTIGEN CLASS I	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									HISTOCOMPATIBILITY ANTIGEN AW68.1 (LEUCOCYTE IHSB 3 ANTIGEN) IHSB 4	
1269	1hbs	A	25	288	0			302.23	HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN AW68.1 (LEUCOCYTE IHSB 3 ANTIGEN) IHSB 4	
1269	1mbe	A	26	285	0	0.70	1.00		HLA CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-E; CHAIN: A; C; BETA-2-MICROGLOBULIN; CHAIN: B; D; PEPTIDE (VMAPTVLL); CHAIN: P; Q;	MAJOR HISTOCOMPATIBILITY COMPLEX MHC NONCLASSICAL CHAIN, MHC-E, HLA-E, MHC CLASS HLA-E, HLA E, MAJOR HISTOCOMPATIBILITY COMPLEX, MHC, HLA, 2 BETA 2 MICROGLOBULIN, PEPTIDE, LEADER PEPTIDE, 3 NON-CLASSICAL MHC, CLASS IB MHC
1269	1mbe	A	26	288	0			253.44	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-E; CHAIN: A; C; BETA-2-MICROGLOBULIN; CHAIN: B; D; PEPTIDE (VMAPTVLL); CHAIN: P; Q;	MAJOR HISTOCOMPATIBILITY COMPLEX MHC NONCLASSICAL CHAIN, MHC-E, HLA-E, MHC CLASS HLA-E, HLA E, MAJOR HISTOCOMPATIBILITY COMPLEX, MHC, HLA, 2 BETA 2 MICROGLOBULIN, PEPTIDE, LEADER PEPTIDE, 3 NON-CLASSICAL MHC, CLASS IB MHC
1269	1qpd	A	26	285	0	0.86	1.00		HISTOCOMPATIBILITY LEUCOCYTE ANTIGEN (HLA)-CW4 CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HLA-CW4 SPECIFIC PEPTIDE; CHAIN: C;	IMMUNE SYSTEM IMMUNOGLOBULIN (IG)-LIKE DOMAIN, ALPHA HELIX, BETA SHEET, 2 IMMUNE SYSTEM

SEQ NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast score	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1269	1tmc	A	25	200	8e-88	0.97	1.00		HISTOCOMPATIBILITY ANTIGEN TRUNCATED HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-A*68 ITMC 3 COMPLEXED WITH A DECAMERIC PEPTIDE (EVAPPEYHRK) ITMC 4	
1269	1tmc	A	25	200	8e-88			257.46	HISTOCOMPATIBILITY ANTIGEN TRUNCATED HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-A*68 ITMC 3 COMPLEXED WITH A DECAMERIC PEPTIDE (EVAPPEYHRK) ITMC 4	
1271	1aln	A	25	218	1.4e-94	0.95	1.00		B*3501; CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C;	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MIC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)
1271	1aln	A	25	219	5.1e-96			239.16	B*3501; CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C;	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MIC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)
1271	1aln	A	26	210	5.1e-96	1.03	1.00		B*3501; CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C;	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MIC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)
1271	1agd	A	25	218	3.2e-95	1.03	1.00		B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B;	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV.

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQOL D score	Compound	PDB annotation
									HIV-1 GAG PEPTIDE (GGKKKKYL - INDEX PEPTIDE); CHAIN: C;	MHC CLASS I, HISTOCOMPATIBILITY COMPLEX
1271	1agd	A	25	219	3.2e-95			243.91	B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKKKKYL - INDEX PEPTIDE); CHAIN: C;	HISTOCOMPATIBILITY COMPLEX B*0801; PEPTIDE HLA B*08, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX
1271	1duz	A	25	218	3.2e-91	0.93	1.00		HLA-A*0201; CHAIN: A, D; BETA-2 MICROGLOBULIN; CHAIN: B, E; HTLV-1 OCTAMERIC TAX PEPTIDE; CHAIN: C, F;	IMMUNE SYSTEM IMMUNOGLOBULIN FOLD
1271	1efx	A	25	218	1.6e-93	0.95	1.00		HLA-CW3 (HEAVY CHAIN); CHAIN: A; BETA-2- MICROGLOBULIN; CHAIN: B; PEPTIDE FROM IMPORTIN ALPHA-2; CHAIN: C; NATURAL KILLER CELL RECEPTOR KIR2DL2; CHAIN: D, E;	IMMUNE SYSTEM MHC HLA, CLASS I, KIR, NK CELL RECEPTOR, IMMUNOGLOBULIN 2 FOLD, RECEPTOR/MHC COMPLEX
1271	1efx	A	26	210	1e-95	1.16	1.00		HLA-CW3 (HEAVY CHAIN); CHAIN: A; BETA-2- MICROGLOBULIN; CHAIN: B; PEPTIDE FROM IMPORTIN ALPHA-2; CHAIN: C; NATURAL KILLER CELL RECEPTOR KIR2DL2; CHAIN: D, E;	IMMUNE SYSTEM MHC HLA, CLASS I, KIR, NK CELL RECEPTOR, IMMUNOGLOBULIN 2 FOLD, RECEPTOR/MHC COMPLEX
1271	1hsa	A	25	218	4.8e-94	0.99	1.00		HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN IHS A 3 /HLA- B*ASTERISK02033 IHS A 4	HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I
1271	1hsa	A	25	219	4.8e-94			235.85	HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fst Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									HISTOCOMPATIBILITY ANTIGEN I HSA 3 /HLA-B*ASERISK27055; I HSA 4	
1271	1hsb	A	25	218	4.8e-92	1.11	1.00		HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN AW68.1 (LEUCOCYTE I HSB 3 ANTIGEN) I HSB 4	
1271	1hsb	A	25	219	4.8e-92			238.32	HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN AW68.1 (LEUCOCYTE I HSB 3 ANTIGEN) I HSB 4	
1271	1mbe	A	26	218	1.6e-92	0.94	1.00		HLA CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-E; CHAIN: A; C; BETA-2-MICROGLOBULIN; CHAIN: B; D; PEPTIDE (VMAPTVLL); CHAIN: P; Q;	MAJOR HISTOCOMPATIBILITY COMPLEX MHC NONCLASSICAL CHAIN, MHC-E, HLA-E, MHC CLASS HLA-E, HLA E, MAJOR HISTOCOMPATIBILITY COMPLEX, MHC, HLA, 2 BETA 2 MICROGLOBULIN, PEPTIDE, LEADER PEPTIDE, 3 NON-CLASSICAL MHC, CLASS IB MHC
1271	1mbe	A	26	219	1.6e-92			218.16	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-E; CHAIN: A; C; BETA-2-MICROGLOBULIN; CHAIN: B; D; PEPTIDE (VMAPTVLL); CHAIN: P; Q;	MAJOR HISTOCOMPATIBILITY COMPLEX MHC NONCLASSICAL CHAIN, MHC-E, HLA-E, MHC CLASS HLA-E, HLA E, MAJOR HISTOCOMPATIBILITY COMPLEX, MHC, HLA, 2 BETA 2 MICROGLOBULIN, PEPTIDE, LEADER PEPTIDE, 3 NON-CLASSICAL MHC, CLASS IB MHC
1271	1ggd	A	26	218	1.6e-92	0.95	1.00		HISTOCOMPATIBILITY	IMMUNE SYSTEM

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									LEUKOCYTE ANTIGEN (HLA)-CW4 CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HLA-CW4 SPECIFIC PEPTIDE; CHAIN: C;	IMMUNOGLOBULIN (IG)-LIKE DOMAIN, ALPHA HELIX, BETA SHEET, 2 IMMUNE SYSTEM
1271	1lmc	A	25	199	1.4e-83			267.94	HISTOCOMPATIBILITY ANTIGEN TRUNCATED HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-AW68 ITMC 3 COMPLEXED WITH A DECAMERIC PEPTIDE (EVAPPEYHRK) ITMC 4	
1272	1aln	A	25	213	8e-91	0.92	1.00		B*3501; CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C;	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)
1272	1aln	A	25	213	8e-91			150.68	B*3501; CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C;	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)
1272	1agd	A	25	213	3.2e-91	0.79	1.00		B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKKYKL - INDEX PEPTIDE); CHAIN: C;	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX
1272	1agd	A	25	213	3.2e-91			152.02	B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKKYKL - INDEX PEPTIDE); CHAIN: C;	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1272	1duz	A	25	213	6.4e-90	0.75	1.00		HLA-A*0201; CHAIN: A, D; BETA-2 MICROGLOBULIN; CHAIN: B, E; HTLV-1 OCTAMERIC TAX PEPTIDE; CHAIN: C, F;	IMMUNE SYSTEM IMMUNOGLOBULIN FOLD
1272	1efx	A	25	213	6.4e-91	0.89	1.00		HLA-CW3 (HEAVY CHAIN); CHAIN: A; BETA-2-MICROGLOBULIN; CHAIN: B; PEPTIDE FROM IMPORTIN ALPHA-2; CHAIN: C; NATURAL KILLER CELL RECEPTOR KIR2DL2; CHAIN: D, E;	IMMUNE SYSTEM MHC, HLA, CLASS I, KIR, NK CELL RECEPTOR, IMMUNOGLOBULIN 2 FOLD, RECEPTOR/MHC COMPLEX
1272	1hsa	A	25	213	1.6e-90	0.92	1.00		HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN IHS A 3/HLA-B*ASTERISK027055 IHS A 4	
1272	1hsa	A	25	213	1.6e-90			151.46	HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN IHS A 3/HLA-B*ASTERISK027055 IHS A 4	
1272	1hsb	A	25	213	3.2e-91	0.87	1.00		HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN AW68.1 (LEUCOCYTE IHSB 3 ANTIGEN) IHSB 4	
1272	1hsb	A	25	213	3.2e-91			178.43	HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN AW68.1 (LEUCOCYTE IHSB 3 ANTIGEN) IHSB 4	

SEQ ID NO.	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1272	1mhe	A	26	213	4.8e-87	0.92	1.00		HLA CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-B; CHAIN: A; C; BETA-2-MICROGLOBULIN; CHAIN: B; D; PEPTIDE (VMAFRTVLL); CHAIN: P; Q;	MAJOR HISTOCOMPATIBILITY COMPLEX MHC NONCLASSICAL CHAIN, MHC-E, HLA-E, MHC CLASS HLA-E, HLA E, MAJOR HISTOCOMPATIBILITY COMPLEX, MHC, HLA, 2 BETA 2, MICROGLOBULIN, PEPTIDE, LEADER PEPTIDE, 3 NON-CLASSICAL MHC, CLASS IB MHC
1272	1mhe	A	26	213	4.8e-87			144.34	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-B; CHAIN: A; C; BETA-2-MICROGLOBULIN; CHAIN: B; D; PEPTIDE (VMAFRTVLL); CHAIN: P; Q;	MAJOR HISTOCOMPATIBILITY COMPLEX MHC NONCLASSICAL CHAIN, MHC-E, HLA-E, MHC CLASS HLA-E, HLA E, MAJOR HISTOCOMPATIBILITY COMPLEX, MHC, HLA, 2 BETA 2, MICROGLOBULIN, PEPTIDE, LEADER PEPTIDE, 3 NON-CLASSICAL MHC, CLASS IB MHC
1272	1ogd	A	26	213	8e-89	0.67	1.00		HISTOCOMPATIBILITY LEUKOCYTE ANTIGEN (HLA)-CW4 CHAIN: A; BETA-2-MICROGLOBULIN; CHAIN: B; HLA-CW4 SPECIFIC PEPTIDE; CHAIN: C;	IMMUNE SYSTEM IMMUNOGLOBULIN (IG)-LIKE DOMAIN, ALPHA HELIX, BETA SHEET, 2 IMMUNE SYSTEM
1272	1ime	A	25	201	9.6e-87	0.83	1.00		HISTOCOMPATIBILITY ANTIGEN TRUNCATED HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-A*W68 1TMC 3 COMPLEXED WITH A DECAMERIC PEPTIDE (EVAPPEYHRK) 1TMC 4	
1272	1ime	A	25	205	9.6e-87			215.19	HISTOCOMPATIBILITY ANTIGEN TRUNCATED	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-A*68 ITMC 3 COMPLEXED WITH A DECA-MERIC PEPTIDE (EVAPPEYHRS) ITMC 4	
1273	1ain	A	25	205	6.4e-97	0.98	1.00		B*3501; CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C;	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)
1273	1ain	A	25	219	6.4e-97			221.84	B*3501; CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C;	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)
1273	1agd	A	25	205	3.2e-97	1.14	1.00		B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKKKKYL - INDEX PEPTIDE); CHAIN: C;	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX
1273	1agd	A	25	219	3.2e-97			223.96	B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKKKKYL - INDEX PEPTIDE); CHAIN: C;	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX
1273	1duz	A	25	205	1.1e-95	1.27	1.00		HLA-A*0201; CHAIN: A, D; BETA-2 MICROGLOBULIN; CHAIN: B; E; HIV-1 OCTAMERIC TAX PEPTIDE; CHAIN: C, F;	IMMUNE SYSTEM IMMUNOGLOBULIN FOLD
1273	1efx	A	25	205	4.8e-97	1.17	1.00		HLA-CW3 (HEAVY CHAIN); CHAIN: A; BETA-2-	IMMUNE SYSTEM MHC, HLA, CLASS I, KIR, NK CELL RECEPTOR,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									MICROGLOBULIN; CHAIN: B; PEPTIDE FROM IMPORIN ALPHA-2; CHAIN: C; NATURAL KILLER CELL RECEPTOR KIR2DL2; CHAIN: D; E;	IMMUNOGLOBULIN 2 FOLD, RECEPTOR/MHC COMPLEX
1273	1hsa	A	25	205	1.6e-96	1.12	1.00		HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN I HSA 3 /HLA-B*ASTERISK27055 I HSA 4	
1273	1hsa	A	25	219	1.6e-96			222.04	HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN I HSA 3 /HLA-B*ASTERISK27055 I HSA 4	
1273	1hsb	A	25	205	1.6e-97	1.03	1.00		HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN A W68.1 (LEUCOCYTE I HSB 3 ANTIGEN) I HSB 4	
1273	1hsb	A	25	218	1.6e-97			245.70	HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN A W68.1 (LEUCOCYTE I HSB 3 ANTIGEN) I HSB 4	
1273	1lqd	A	26	205	1.1e-95	1.07	1.00		HISTOCOMPATIBILITY LEUCOCYTE ANTIGEN (HLA)-CW4 CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HLA-CW4 SPECIFIC PEPTIDE; CHAIN: C	IMMUNE SYSTEM IMMUNOGLOBULIN (IG)-LIKE DOMAIN, ALPHA HELIX; BETA SHEET, 2 IMMUNE SYSTEM
1273	1lmc	A	25	199	1.6e-93	1.25	1.00		HISTOCOMPATIBILITY	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									ANTIGEN TRUNCATED HUMAN CLASS 1 HISTOCOMPATIBILITY ANTIGEN HLA-A*68 ITMC 3 COMPLEXED WITH A DECA-MERIC PEPTIDE (EVAPPEYHRK) ITMC 4	
1273	1tmc	A	25	199	1.6e-93			273.81	ANTIGEN TRUNCATED HUMAN CLASS 1 HISTOCOMPATIBILITY ANTIGEN HLA-A*68 ITMC 3 COMPLEXED WITH A DECA-MERIC PEPTIDE (EVAPPEYHRK) ITMC 4	
1274	1huo	A	1	126	1.6e-22	0.30	1.00		PROMYELOCYTIC LEUKEMIA ZINC FINGER PROTEIN PLZF; CHAIN: A;	GENE REGULATION POZ DOMAIN; PROTEIN-PROTEIN INTERACTION DOMAIN, TRANSCRIPTIONAL 2 REPRESSOR, ZINC-FINGER PROTEIN, X-RAY CRYSTALLOGRAPHY, 3 PROTEIN STRUCTURE, PROMYELOCYTIC LEUKEMIA, GENE REGULATION
1274	1huo	A	5	128	3.4e-28	0.41	0.99		PROMYELOCYTIC LEUKEMIA ZINC FINGER PROTEIN PLZF; CHAIN: A;	GENE REGULATION POZ DOMAIN; PROTEIN-PROTEIN INTERACTION DOMAIN, TRANSCRIPTIONAL 2 REPRESSOR, ZINC-FINGER PROTEIN, X-RAY CRYSTALLOGRAPHY, 3 PROTEIN STRUCTURE, PROMYELOCYTIC LEUKEMIA, GENE REGULATION
1274	1goi		291	438	1.1e-11	0.05	0.17		OXIDOREDUCTASE/OXYGEN(A) GALACTOSE OXIDASE	

SEQ NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fsi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1274	1gof		383	495	1.6e-08	0.27	0.13		(E.C.1.1.3.9) (PH 4.5) IGF 3 OXIDOREDUCTASE(OXYGEN(A)) GALACTOSE OXIDASE (E.C.1.1.3.9) (PH 4.5) IGF 3	
1275	1eun	A	170	385	6.8e-09			65.74	ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 22 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1275	1quu	A	180	415	3.4e-12			59.43	HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL.
1275	1sig		130	416	5.1e-05			76.16	RNA POLYMERASE PRIMARY SIGMA FACTOR; CHAIN: NULL;	TRANSCRIPTION REGULATION SIGMA 70; RNA POLYMERASE SIGMA FACTOR, TRANSCRIPTION REGULATION
1276	1abr	B	413	552	1.4e-09	0.45	0.40		COMPLEX (GLYCOSIDASE/CARBOHYDRATE) ABRIN-A COMPLEXED WITH TWO SUGAR CHAINS IABR 3	
1276	1ec7	B	441	552	1.2e-15	0.16	0.21		RIPOSONE-INACTIVATING PROTEIN TYPE II; CHAIN: A; RIPOSONE-INACTIVATING PROTEIN TYPE II; CHAIN: B	RIPOSONE RIPOSONE-INACTIVATING PROTEIN TYPE II
1276	1ec7	B	450	543	0.00011	-0.25	0.13		RIPOSONE-INACTIVATING PROTEIN TYPE II; CHAIN: A; RIPOSONE-INACTIVATING PROTEIN TYPE II; CHAIN: B	RIPOSONE RIPOSONE-INACTIVATING PROTEIN TYPE II
1276	1gqg	A	123	345	6.4e-22	0.09	0.28		SPORE COAT POLYSACCHARIDE BIOSYNTHESIS PROTEIN	TRANSFERASE GLYCOSYLTRANSFERASE

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fst Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1276	1xyf	A	441	543	1.6e-16	-0.02	0.66		CHAIN: A; ENDO-1,4-BETA-XYLANASE;	HYDROLASE XYLAN DEGRADATION
1276	2aal	B	441	543	1.3e-07	-0.31	0.03		CHAIN: A, B; GLYCOSIDASE RICIN (E.C.3.2.2.2) 2A1 3	
1279	2ak3	A	1	38	1.3e-16	-0.87	0.98		TRANSFERASE (PHOSPHOTRANSFERASE) ADENYLATE KINASE ISOENZYME-3 (GTP: AMP PHOSPHOTRANSFERASE) 2AK3 3 (E.C.2.7.4.10) 2AK3 4	
1280	12e8	H	59	253	1.3e-38	0.01	0.21		2E8 (GGI=KAPPA+) ANTIBODY; CHAIN: L, H, M, P;	IMMUNOGLOBULIN
1280	1a0q	H	50	254	6.4e-37			61.67	29G11 FAB; CHAIN: L, H;	IMMUNOGLOBULIN
1280	1a0q	H	59	253	6.4e-37	-0.31	0.27		29G11 FAB; CHAIN: L, H;	CATALYTIC ANTIBODY, ESTERASE
1280	1a3r	H	50	256	1.3e-36			60.58	IGG2A; CHAIN: L, H; HUMAN RHINOVIRUS CAPSID PROTEIN VP2; CHAIN: P;	CATALYTIC ANTIBODY, ESTERASE COMPLEX (IMMUNOGLOBULIN/VIRAL PEPTIDE) ANTIBODY 8F5; IMMUNOGLOBULIN, ANTIBODY; RHINOVIRUS, NEUTRALIZATION, 2 CONTINUOUS EPTOPE, COMPLEX (IMMUNOGLOBULIN/VIRAL PEPTIDE)
1280	1a4j	L	51	252	9.6e-37	-0.11	0.17		IMMUNOGLOBULIN; DIELS ALDER CATALYTIC ANTIBODY; CHAIN: L, H, A, B;	IMMUNOGLOBULIN, ANTIBODY; CATALYTIC ANTIBODY, DIELS ALDER, 2 GERMLINE
1280	1a5f	H	48	256	3.2e-35			61.06	MONOCLONAL ANTI-E-SELECTIN 7A9 ANTIBODY; CHAIN: L, H;	IMMUNOGLOBULIN, FAB, ANTIBODY, ANTI-E-SELECTIN

SEQ NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pst Blast score	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1280	1adq	L	50	255	1.1e-37	-0.04	0.00		IGG1 REA; CHAIN: A; RE-AN IGM/LAMBDA; CHAIN: H, L;	COMPLEX (IMMUNOGLOBULIN/AUTOANTIGEN) COMPLEX (IMMUNOGLOBULIN/AUTOANTIGEN) RHEUMATOID FACTOR 2 AUTO- ANTIBODY COMPLEX COMPLEX (VIRAL CAPSID/IMMUNOGLOBULIN) HIV-1 CA, HIV CA, HIV P24, P24; FAB, FAB LIGHT CHAIN, FAB HEAVY CHAIN COMPLEX (VIRAL CAPSID/IMMUNOGLOBULIN), HIV, CAPSID PROTEIN, 2 P24 IMMUNOGLOBULIN IMMUNOGLOBULIN; ANTIBODY FAB, CATALYST, ALDOLASE REACTION IMMUNE SYSTEM IMMUNOGLOBULIN; IMMUNOGLOBULIN ANTIBODY ENGINEERING, HUMANIZED AND CHIMERIC ANTIBODY, FAB, 2 X- RAY STRUCTURE, THREE- DIMENSIONAL STRUCTURE, GAMMA-3 INTERFERON, IMMUNE SYSTEM
1280	1afv	H	52	253	4.8e-37	0.08	0.58		HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 CAPSID CHAIN: A, B; ANTIBODY FAB253 FRAGMENT; CHAIN: H, K, L, M;	
1280	1axt	H	51	256	4.8e-33			56.82	IMMUNOGLOBULIN IGG2A; CHAIN: L, H;	
1280	1b2w	L	51	258	8e-39	0.04	-0.07		ANTIBODY (LIGHT CHAIN); CHAIN: L; ANTIBODY (HEAVY CHAIN); CHAIN: H;	
1280	1b4j	L	51	258	1.4e-37	0.00	0.09		ANTIBODY; CHAIN: L, H;	ANTIBODY ENGINEERING HUMANIZED AND CHIMERIC ANTIBODIES 2 FAB, X-RAY STRUCTURES, GAMMA- INTERFERON IMMUNOGLOBULIN IMMUNOGLOBULIN, KAPPA LIGHT-
1280	1b6d	A	51	252	4.8e-37	-0.12	0.13		IMMUNOGLOBULIN; CHAIN: A; B;	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fst Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1280	1bjt	L	51	252	8e-18	0.09	-0.09		FAB FRAGMENT; CHAIN: L, H, I, K; VASCULAR ENDOTHELIAL GROWTH FACTOR; CHAIN: V, W;	CHAIN DIMER HEADER COMPLEX (ANTIBODY/ANTIGEN) FAB-12: VEGF: COMPLEX (ANTIBODY/ANTIGEN), ANGIOGENIC FACTOR
1280	1bin	A	47	252	4.8e-35			57.09	MONOCLONAL ANTIBODY MRK-16 (LIGHT CHAIN); CHAIN: A, C; MONOCLONAL ANTIBODY MRK-16 (HEAVY CHAIN); CHAIN: B, D;	IMMUNE SYSTEM IMMUNOGLOBULIN, IMMUNE SYSTEM
1280	1bm3	H	51	258	1.6e-34			57.73	IMMUNOGLOBULIN OPG2 FAB; CONSTANT DOMAIN; CHAIN: L; IMMUNOGLOBULIN OPG2 FAB; VARIABLE DOMAIN; CHAIN: H;	IMMUNE SYSTEM IMMUNOGLOBULIN
1280	1bof	H	50	255	3.2e-36			59.53	COMPLEX (ANTIBODY/ANTIGEN) HYHEL-3 FAB COMPLEXED WITH BOBWHITE QUAIL LYSOZYME BQ.3 1BQL 95	
1280	1bz7	B	51	250	1.6e-26			57.49	ANTIBODY R24 (LIGHT CHAIN); CHAIN: A; ANTIBODY R24 (HEAVY CHAIN); CHAIN: B;	IMMUNE SYSTEM ANTIBODY (FAB FRAGMENT), IMMUNE SYSTEM
1280	1ce1	L	51	252	9.6e-37	0.11	-0.03		CAMPATH-1HLIGHT CHAIN; CHAIN: L; CAMPATH-1HHEAVY CHAIN; CHAIN: H; PEPTIDE ANTIGEN; CHAIN: P;	ANTIBODY THERAPEUTIC, ANTIBODY, CD52
1280	1cr9	H	59	255	8e-39	-0.12	0.60		FAB ANTIBODY LIGHT CHAIN; CHAIN: L; FAB ANTIBODY HEAVY CHAIN; CHAIN: H;	IMMUNE SYSTEM ANTI-PRION FAB 3F4; ANTI-PRION FAB 3F4 ANTI-PRION ANTIBODY; FAB 3F4
1280	1fb1	H	48	255	1.6e-36			56.80	COMPLEX (ANTIBODY/ANTIGEN) FAB FRAGMENT OF THE	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									MONOCLONAL ANTIBODY P9.13.7 (IGG1) IFBI 3 COMPLEXED WITH LYSOZYME (E.C.3.2.1.17) IFBI 4	
1280	1fr	H	51	256	3.2e-33			56.39	4.4-20 (GT'G2A* κ APPAS) FAB FRAGMENT; IFLR 5 CHAIN: L _h , H _h IFLR 6	IMMUNOGLOBULIN
1280	1fd	A	51	258	1.4e-37	0.11	-0.12		IMMUNOGLOBULIN FAB FRAGMENT OF HUMANIZED ANTIBODY 4D5, VERSION 4 IFVD 3	
1280	1fd	B	51	258	6.4e-32			57.20	IMMUNOGLOBULIN FAB FRAGMENT OF HUMANIZED ANTIBODY 4D5, VERSION 4 IFVD 3	
1280	lhyx	L	47	255	1.3e-34			57.33	IMMUNOGLOBULIN 6D9; CHAIN: L _h , H _h	CATALYTIC ANTIBODY CATALYTIC ANTIBODY 6D9 CATALYTIC ANTIBODY, ESTER HYDROLYSIS, ESTEROLYTIC, FAB, 2 IMMUNOGLOBULIN
1280	liat	H	48	254	4.8e-33			60.65	IDIOTYPIC FAB 730.1.4 (IGG1) OF VIRUS 11A1 5 CHAIN: L _h , H _h ; 11A1 7 ANTI-IDIOTYPIC FAB 409.5.3 (IGG2A); 11A1 9 CHAIN: M _h , I 11A1 10	COMPLEX (IMMUNOGLOBULIN IGG1/IGG2A)
1280	lige	H	51	258	1.0e-32			57.26	COMPLEX (ANTIBODY/BINDING PROTEIN) IGG1 FAB FRAGMENT COMPLEXED WITH PROTEIN G (DOMAIN IID) IGC-5 PROTEIN G; STREPTOCOCCUS IGC 15	
1280	ligf	L	47	258	8e-35			58.26	IMMUNOGLOBULIN IGG1 FAB FRAGMENT (B1312) IIGF 3	

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1280	1lg1	B	59	253	1.6e-36	0.02	0.37		IGG1 INTACT ANTIBODY MAB61.1.3; CHAIN: A, B, C, D	IMMUNOGLOBULIN, V REGION, C REGION, HINGE REGION
1280	1le1	H	51	255	6.4e-34			57.31	28B4 FAB; CHAIN: L, H;	CATALYTIC ANTIBODY SULFIDE OXIDATION, MONOOXYGENASE, OXYGENATION, FAB, 2 IMMUNOGLOBULIN, CATALYTIC ANTIBODY
1280	1mlb	B	48	258	8e-36			56.48	IMMUNOGLOBULIN FAB D44.1 (IGG1,KAPPA)(BALB/C MOUSE, MONOCLONAL ANTIBODY) 1MLB 5	
1280	1lnc		178	254	0.0015	0.08	0.35		TITIN; CHAIN: NULL;	MUSCLE PROTEIN CONNECTIN, NEXTIN; CELL ADHESION, GLYCOPROTEIN, TRANSMEMBRANE, REPEAT, BRAIN, 2 IMMUNOGLOBULIN FOLD, ALTERNATIVE SPLICING, SIGNAL, 3 MUSCLE PROTEIN
1280	1lup	H	51	253	6.4e-37	-0.09	0.22		NIG9 (IGG1-LAMBDA-); CHAIN: L, H;	IMMUNOGLOBULIN
1280	1sm3	H	51	256	1.6e-36			58.83	SM3 ANTIBODY; CHAIN: L, H; PEPTIDE EPITOPE; CHAIN: P; PEPTIDE EPITOPE; CHAIN: P;	COMPLEX (ANTIBODY/PEPTIDE EPITOPE) ANTIBODY, PEPTIDE ANTIGEN, ANTITUMOR ANTIBODY, 2 COMPLEX (ANTIBODY/PEPTIDE EPITOPE)
1280	1sm3	H	59	253	1.6e-36	-0.09	0.41		SM3 ANTIBODY; CHAIN: L, H; PEPTIDE EPITOPE; CHAIN: P;	COMPLEX (ANTIBODY/PEPTIDE EPITOPE) ANTIBODY, PEPTIDE ANTIGEN, ANTITUMOR ANTIBODY, 2 COMPLEX (ANTIBODY/PEPTIDE EPITOPE)
1280	1sm3	L	50	252	3.2e-30			56.66	SM3 ANTIBODY; CHAIN: L, H; PEPTIDE EPITOPE; CHAIN: P;	COMPLEX (ANTIBODY/PEPTIDE EPITOPE) ANTIBODY, PEPTIDE ANTIGEN, ANTITUMOR ANTIBODY,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
1280	1tet	H	48	256	6.4e-36			57.32	IMMUNOGLOBULIN IGG1 MONOCLONAL FAB FRAGMENT (TE33) COMPLEX WITH CHOLERA (TET 3 TOXIN PEPTIDE 3 (CTP3), TET 4	2 COMPLEX (ANTIBODY/PEPTIDE EPITOPE)
1280	1nm		178	254	0.0051	-0.05	0.05		MUSCLE PROTEIN TITIN MODULE M5 (CONNECTIN) ITNM 3 (NMR, MINIMIZED AVERAGE STRUCTURE) ITNM 4 ITNM 58	
1280	1wej	H	59	253	3.2e-37	0.55	0.70		E8 ANTIBODY; CHAIN: L, H; CYTOCHROME C; CHAIN: F;	COMPLEX (ANTIBODY/ELECTRON TRANSPORT) FAB E8; CYT C, ANTIGEN: IMMUNOGLOBULIN, IGG1 KAPPA, FAB FRAGMENT, HORSE 2 CYTOCHROME C, COMPLEX (ANTIBODY/ELECTRON TRANSPORT)
1280	1wvc	A	164	254	0.0051	-0.18	0.01		NT-3 GROWTH FACTOR RECEPTOR TRKC; CHAIN: A;	TRANSFERASE TRK RECEPTOR, RECEPTOR TYROSINE KINASE, 3D-DOMAIN SWAPPING, 2 TRANSFERASE
1280	2sc8	H	48	254	1.1e-37			57.06	IGG 508; CHAIN: L, H;	CATALYTIC ANTIBODY CLOSURE REACTION
1280	2sc8	H	59	253	1.1e-37	0.11	0.53		IGG 508; CHAIN: L, H;	CATALYTIC ANTIBODY CLOSURE REACTION
1280	2cgr	H	51	254	1.6e-31			57.12	IMMUNOGLOBULIN (GQ2B (KAPPA) FAB FRAGMENT COMPLEXED WITH ANTIGEN 2CGR 3 N-(p-CYANOPHENYL)-N-(DIHENYLMETHYL)	CATALYTIC ANTIBODY, FAB, RING CLOSURE REACTION

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1280	2fgw	L	51	258	1.6e-38	0.00	-0.08		GUANIDINEACETIC ACID 2CGR 4	
1280	2hml	C	47	258	4.8e-33			56.78	IMMUNOGLOBULIN FAB FRAGMENT OF A HUMANIZED VERSION OF THE ANTI-CD18 2FGW 3 ANTIBODY 'H52' (HUH52-OZ FAB) 2FGW 4	COMPLEX (RT/DNA/FAB) HIV-1 RT; FAB 28; AIDS; HIV-1, RT; POLYMERASE
1280	7fmb	H	49	255	3.2e-31			57.01	HIV-1 REVERSE TRANSCRIPTASE; CHAIN: A, B; MONOCLONAL ANTIBODY 28; CHAIN: C, D; DNA; CHAIN: E, F; IMMUNOGLOBULIN	
1284	1erk	A	1	46	3.2e-19	-0.83	0.27		IMMUNOGLOBULIN FAB NEW (LAMBDA LIGHT CHAIN) 7FAB 3	
1284	1qb4	A	1	46	4.8e-19	-0.83	0.30		CREATINE KINASE; CHAIN: A, B, C, D; CREATINE KINASE, BRAIN-TYPE	TRANSFERASE TRANSFERASE, CREATINE KINASE
1284	1qk1	A	1	46	6.4e-19	-0.83	0.33		CREATINE KINASE, B CHAIN; CHAIN: A, B, C, D; CREATINE KINASE, CANCER, CELLULAR ENERGY 2 METABOLISM, GUANIDINO KINASE, NEURODEGENERATIVE DISORDERS	TRANSFERASE BB-CK, BRAIN-TYPE CREATINE KINASE; BRAIN-TYPE CREATINE KINASE, CANCER, CELLULAR ENERGY 2 METABOLISM, GUANIDINO KINASE, NEURODEGENERATIVE DISORDERS
1284	2ark	A	1	46	1.4e-19	-0.83	0.19		CREATINE KINASE; CHAIN: A; CREATINE KINASE, CANCER, CELLULAR ENERGY 2 METABOLISM, GUANIDINO KINASE, MITOCHONDRIAL PERMEABILITY 3 TRANSITION, OCTAMER STABILITY	TRANSFERASE (CREATINE KINASE) UMTCK, MIA-CK; MITOCHONDRIAL CREATINE KINASE, CANCER, CELLULAR ENERGY 2 METABOLISM, GUANIDINO KINASE, MITOCHONDRIAL PERMEABILITY 3 TRANSITION, OCTAMER STABILITY

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
										TRANSFERASE
1287	1bq0		5	69	1.1e-27	0.89	1.00		DNAJ; CHAIN: NULL;	CHAPERONE HSP40; CHAPERONE, HEAT SHOCK, PROTEIN FOLDING, DNAK
1287	1bq0		5	78	1.1e-27			68.92	DNAJ; CHAIN: NULL;	CHAPERONE HSP40; CHAPERONE, HEAT SHOCK, PROTEIN FOLDING, DNAK
1287	1hdj		10	77	3.4e-30	0.77	1.00		HUMAN HSP40; CHAIN: NULL;	MOLECULAR CHAPERONE HDJ-1; MOLECULAR CHAPERONE
1287	1hdj		5	80	3.4e-30			83.03	HUMAN HSP40; CHAIN: NULL;	MOLECULAR CHAPERONE HDJ-1; MOLECULAR CHAPERONE
1287	1hdj		7	69	1.6e-27	1.26	1.00		HUMAN HSP40; CHAIN: NULL;	MOLECULAR CHAPERONE HDJ-1; MOLECULAR CHAPERONE
1292	1pbw	A	112	300	6.4e-08			93.22	PHOSPHATIDYLINOSITOL 3-KINASE; CHAIN: A, B;	PHOSPHOTRANSFERASE RHOGAP DOMAIN; PHOSPHOTRANSFERASE, TPASE ACTIVATING PROTEIN, GAP, CDC42, 2 PHOSPHOINOSITIDE 3-KINASE, SEB DOMAIN, SH2 DOMAIN, 3 SIGNAL
1292	1pbw	B	112	314	8e-09			94.15	PHOSPHATIDYLINOSITOL 3-KINASE; CHAIN: A, B;	PHOSPHOTRANSFERASE RHOGAP DOMAIN; PHOSPHOTRANSFERASE, TPASE ACTIVATING PROTEIN, GAP, CDC42, 2 PHOSPHOINOSITIDE 3-KINASE, SEB DOMAIN, SH2 DOMAIN, 3 SIGNAL
1292	1rtp		99	288	4.8e-17			109.76	RHOGAP; CHAIN: NULL;	G-PROTEIN CDC42 GTPASE-ACTIVATING PROTEIN; G-PROTEIN, GAP, SIGNAL-TRANSDUCTION
1292	1rx4	A	105	302	1.1e-17			114.46	P50-RHOGAP; CHAIN: A; TRANSFORMING PROTEIN	COMPLEX(GTPASE ACTIVATIN/PROTO-ONCOGENE)

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									RHOA; CHAIN: B;	GTPASE-ACTIVATING PROTEIN RHO GAP; COMPLEX (GTPASE ACTIVATION/PROTO-ONCOGENE) GTPASE, 2 TRANSITION STATE, GAP
1293	1boq	M	112	281	9.6e-54			103.34	MEMBRANE-TYPE MATRIX METALLOPROTEINASE; CHAIN: M; METALLOPROTEINASE INHIBITOR; CHAIN: T;	COMPLEX (METALLOPROTEINASE/RECEPTOR) CDMT1-MMP; TMP-2 MATRIX METALLOPROTEINASE; TISSUE INHIBITOR OF 2 METALLOPROTEINASES; PROTEINASE COMPLEX, PRO- GELATINASE A.3 ACTIVATOR, CRYSTAL-STRUCTURE, COMPLEX 4 (METALLOPROTEINASE/RECEPTOR)
1293	1ege		110	254	8e-60			120.96	HYDROLASE (METALLOPROTEINASE) COLLAGENASE (EC 3.4.24.7) (CATALYTIC DOMAIN) CRYSTAL FORM I ICGE 3	
1293	1eiz	A	107	272	4.8e-63			132.96	STROMELYSIN-1; CHAIN: A;	METALLOPROTEINASE MATRIX METALLOPROTEINASE-3; MATRIX METALLOPROTEINASE, MMP-3, NON-PEPTIDE INHIBITOR
1293	1ek7	A	25	699	0			647.13	GELATINASE A; CHAIN: A;	HYDROLASE MMP-2, 72KD TYPE IV COLLAGENASE; HYDROLASE (METALLOPROTEINASE), FULL-LENGTH, METALLOPROTEINASE, 2 GELATINASE A
1293	1exw	A	274	333	9.6e-14			90.80	HUMAN MATRIX METALLOPROTEINASE 2; CHAIN: A;	HYDROLASE COL-2; BETA SHEET, ALPHA HELIX, HYDROLASE
1293	1fbl		107	449	3.2e-70			151.00	FIBROBLAST (INTERSTITIAL)	METALLOPROTEINASE

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1293	1gem		474	699	9.6e-50			99.59	COLLAGENASE (MMP-1); IFBL 4 CHAIN; NULL; IFBL 5 GELATINASE A; CHAIN: NULL;	HYDROLASE (METALLOPROTEASE) MMP-2, 72KD TYPE IV COLLAGENASE; HYDROLASE, HEMOPLEXIN DOMAIN, HYDROLASE, METALLOPROTEASE
1293	1hfc		115	265	8e-60			117.07	METALLOPROTEASE FIBROBLAST COLLAGENASE (EC 3.4.24.7) IHEC 3	
1293	1mmq		107	279	8e-56			119.28	MATRILYSIN; IMMQ 5 CHAIN: NULL; IMMQ 6	METALLOPROTEASE MMP-9, PUMP-1, MATRIX; IMMQ 7
1293	1pex		477	699	4.8e-63			84.70	COLLAGENASE-3; CHAIN: NULL;	METALLOPROTEASE MMP-13; C-TERMINAL HEMOPLEXIN-LIKE DOMAIN OF MATRIX.
1293	1qib	A	112	272	1.6e-57			144.06	GELATINASE A; CHAIN: A;	METALLOPROTEINASE
										HYDROLASE MATRIX
										METALLOPROTEINASE-2; INHIBITOR, MATRIKXIN, MATRIX
										METALLOPROTEINASE-2 (MMP-2), 2 GELATINASE A, METZINCIN, HYDROLASE
1293	1slm		44	272	1.6e-82			187.06	STROMELYSIN-1; CHAIN: NULL;	HYDROLASE MATRIX
										METALLOPROTEINASE-3, PROTEOGLYCANASE; HYDROLASE, METALLOPROTEINASE, FIBROBLAST, COLLAGEN DEGRADATION
1293	830c	A	107	267	1.6e-59			138.28	MMP-13; CHAIN: A, B;	MATRIX METALLOPROTEASE
										MMP-13; MATRIX
										METALLOPROTEASE
1294	1ck7	A	25	432	0			419.38	GELATINASE A; CHAIN: A;	HYDROLASE MMP-2, 72KD TYPE IV COLLAGENASE; HYDROLASE (METALLOPROTEASE), FULL-

SEQ ID NO:	PDB ID	CHAIN	STAR T AA	END AA	PstBlast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1294	1exw	A	274	333	3.2e-21			90.47	HUMAN MATRIX METALLOPROTEINASE 2; CHAIN: A;	LENGTH, METALLOPROTEINASE, 2 GELATINASE A HYDROLASE COL-2 BETA SHEET, ALPHA HELIX, HYDROLASE
1297	2ucz		400	562	3.2e-44			80.92	UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	UBIQUITIN CONJUGATION UBC7; UBIQUITIN CONJUGATION, LIGASE, YEAST
1298	1b1h	A	1462	1834	8e-44			176.45	HEMOLIN; CHAIN: A, B;	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION CELL ADHESION PROTEIN RGD, EXTRACELLULAR MATRIX IFN γ 18
1298	1fnt		1660	2042	8e-18			104.50	FIBRONECTIN; IFN γ 6 CHAIN: NULL; IFN γ 7	COMPLEX (IMMUNOGLOBULIN/RECEPTOR) IMMUNOGLOBULIN FOLD, TRANSMEMBRANE GLYCOPROTEIN RECEPTOR, 2 SIGNAL, COMPLEX (IMMUNOGLOBULIN/RECEPTOR)
1298	11th	B	1370	1645	3.2e-18			104.57	INTERLEUKIN-1 BETA; CHAIN: A; TYPE 1 INTERLEUKIN-1 RECEPTOR; CHAIN: B;	
1301	1agr	E	45	172	4.8e-48			146.45	GUANINE NUCLEOTIDE-BINDING PROTEIN G0; CHAIN: A, D; RGS4; CHAIN: E, H;	COMPLEX (SIGNAL TRANSDUCTION/REGULATOR) GL- ALPHA-1; REGULATOR OF G- PROTEIN SIGNALING 4; GL-ALPHA- 1, HYDROLASE, SIGNAL TRANSDUCTION, RGS4, 2 COMPLEX (SIGNAL TRANSDUCTION/REGULATOR), GTP-BINDING, 3 GTPASE ACTIVATING PROTEIN COMPLEX (SIGNAL)
1301	1agr	H	54	169	6.4e-43			133.76	GUANINE NUCLEOTIDE-	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									BINDING PROTEIN GQ; CHAIN: A, D; RGS4; CHAIN: E, H;	TRANSDUCTION/REGULATOR) G1-ALPHA-1; REGULATOR OF G-PROTEIN SIGNALING 4; G1-ALPHA-1, HYDROLASE, SIGNAL TRANSDUCTION, RGS4, 2 COMPLEX (SIGNAL TRANSDUCTION/REGULATOR), GTP-BINDING, 3 GTPASE ACTIVATING PROTEIN
1301	1cmz	A	46	172	3.2e-46			121.40	GAP (G-ALPHA INTERACTING) PROTEIN; CHAIN: A;	SIGNALING PROTEIN REGULATION GALPHA INTERACTING PROTEIN; GAP, RGS, REGULATOR OF G PROTEIN, SIGNALING PROTEIN 2 REGULATION
1302	1a4i	A	5	235	4.8e-74			94.97	METHYLENETETRAHYDROFOLATE DEHYDROGENASE / CHAIN: A, B;	OXIDOREDUCTASE METHYLENETETRAHYDROFOLATE DEHYDROGENASE / METHYLENETETRAHYDROFOLATE DEHYDROGENASE, BIFUNCTIONAL, CYCLOHYDROLASE, FOLATE, 2 OXIDOREDUCTASE, HEAD
1302	1b0a	A	1	235	8e-77			106.54	FOLD BIFUNCTIONAL PROTEIN; CHAIN: A;	OXIDOREDUCTASE, HYDROLASE FOLATE, DEHYDROGENASE, BIFUNCTIONAL, 2 CHANNELING, OXIDOREDUCTASE, HYDROLASE
1307	1awc	B	13	157	8e-34	-0.23	0.52		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABP ALPHA; GABP BETA 1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING,

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1307	lawe	B	3	125	4.8e-29	-0.09	0.29		G4 BINDING PROTEIN ALPHA; CHAIN: A; G4 BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GAB/ALPHA; GAB/BETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA) DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1307	1bd8		21	160	8e-27	-0.01	0.19		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1307	1bi7	B	443	560	6.4e-17	0.14	0.04		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; MULTIPLE TUMOR SUPPRESSOR; CHAIN: B;	COMPLEX (KINASE/ANTI-ONCOGENE) CDK6; P19INK4A, MTS1; CYCLIN DEPENDENT KINASE, CYCLIN DEPENDENT KINASE INHIBITORY 2 PROTEIN, CDK, INK4, CELL CYCLE, MULTIPLE TUMOR SUPPRESSOR, 3 MTS1, COMPLEX (KINASE/ANTI-ONCOGENE) HEADER
1307	1bk	B	21	160	6.4e-26	-0.17	0.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1307	1bk	B	50	183	1.3e-23	0.01	0.37		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1307	1bu9	A	1	130	6.4e-25	-0.12	0.15		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	(INHIBITOR PROTEIN KINASE) HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C; TUMOR, SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR, SIGNALING PROTEIN HELIX-TURN-HELIX, ANKYRIN REPEAT
1307	1d9s	A	443	567	1.6e-17	0.14	0.06		CYCLIN-DEPENDENT KINASE 4 INHIBITOR B; CHAIN: A;	CELL CYCLE INHIBITOR P18-INK4C(NK6); CELL CYCLE INHIBITOR, P18-INK4C(NK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
1307	1iib	A	18	161	1.3e-25	-0.12	0.10		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18-INK4C(NK6); CELL CYCLE INHIBITOR, P18-INK4C(NK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
1307	1iib	A	1	129	3.2e-24	0.01	0.37		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18-INK4C(NK6); CELL CYCLE INHIBITOR, P18-INK4C(NK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
1307	1myo		19	127	1.6e-20	0.14	0.01		MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT
1314	1by2		26	138	1.1e-44			112.99	MAC-2 BINDING PROTEIN; CHAIN: NULL;	EXTRACELLULAR MODULE TUMOR-ASSOCIATED ANTIGEN 90K; EXTRACELLULAR MODULE, SCAVENGER RECEPTOR, TUMOUR-ASSOCIATED 2 ANTIGEN, EXTRACELLULAR MATRIX, GLYCOSYLATED PROTEIN
1315	1ae1	A	34	304	1.6e-66			75.73	TROPINONE REDUCTASE-I; CHAIN: A, B;	OXIDOREDUCTASE OXIDOREDUCTASE, TROPANE ALKALOID BIOSYNTHESIS, REDUCTION OF 2 TROPINONE TO TROPINE, SHORT-CHAIN

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1315	1ae1	B	34	304	9.6e-68			76.92	TROPINONE REDUCTASE-I; CHAIN: A, B;	DEHYDROGENASE OXIDOREDUCTASE OXIDOREDUCTASE, TROPANE ALKALOID BIOSYNTHESIS REDUCTION OF 2 TROPINONE TO TROPINE, SHORT-CHAIN DEHYDROGENASE
1315	1bdb		35	314	1.6e-47			65.57	CIS-BIPHENYL-2,3-DIHYDRODIOL-2,3-DEHYDROGENASE; CHAIN: NULL;	OXIDOREDUCTASE NAD-DEPENDENT OXIDOREDUCTASE, SHORT-CHAIN ALCOHOL 2 DEHYDROGENASE, PCB DEGRADATION
1315	1cyl	A	35	297	3.2e-54			69.13	CARBONYL REDUCTASE; CHAIN: A, B, C, D;	OXIDOREDUCTASE SHORT-CHAIN DEHYDROGENASE, OXIDOREDUCTASE
1315	1fdd		38	319	4.8e-32			79.80	17-BETA-HYDROXYSTEROID-DEHYDROGENASE; CHAIN: NULL;	DEHYDROGENASE DEHYDROGENASE, 17-BETA-HYDROXYSTEROID
1315	1fmc	A	30	298	6.4e-66			82.26	7 ALPHA-HYDROXYSTEROID DEHYDROGENASE; CHAIN: A, B;	OXIDOREDUCTASE SHORT-CHAIN DEHYDROGENASE/REDUCTASE, BILE ACID CATABOLISM
1315	1hde	A	35	306	4.8e-67			74.82	OXIDOREDUCTASE 3-ALPHA, 20-BETA-HYDROXYSTEROID DEHYDROGENASE (E.C.1.1.1.53) IHDC 3 COMPLEXED WITH CARBENOXOLONE IHDC 4	
1315	1oaa		35	297	3.2e-21			65.22	SEPIAPTERIN REDUCTASE; CHAIN: NULL;	OXIDOREDUCTASE SEPIAPTERIN REDUCTASE, TETRANHYDROBIOPTERIN, OXIDOREDUCTASE
1315	1ybv	A	24	308	3.2e-61			82.44	TRIHYDROXYNAPHTHALENE REDUCTASE; CHAIN: A, B;	OXIDOREDUCTASE NAPHTHOL REDUCTASE; OXIDOREDUCTASE
1315	2ae2	A	32	291	9.6e-65			76.67	TROPINONE REDUCTASE-II;	OXIDOREDUCTASE

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									CHAIN: A, B;	OXIDOREDUCTASE, TROPANE ALKALOID BIOSYNTHESIS, REDUCTION OF 2 TROPINONE TO PSEUDOTROPINE, SHORT-CHAIN DEHYDROGENASE
1321	1pbk		224	339	1.3e-24			194.11	FKBP25; CHAIN: NULL;	ISOMERASE FKBP25 C-TERMINAL DOMAIN; FKBP12 HOMOLOGOUS DOMAIN OF FKBP25, ISOMERASE
1323	1am4	D	31	218	3.2e-43			50.20	P50-RHO GAP; CHAIN: A, B, C; CDC42HS; CHAIN: D, E, F;	COMPLEX (GTPASE-ACTIVATING/GTP-BINDING) COMPLEX (GTPASE-ACTIVATING/GTP-BINDING), GTPASE ACTIVATION
1323	1byu	A	29	244	3.2e-32			61.74	GTP-BINDING PROTEIN RAN; CHAIN: A, B;	TRANSPORT PROTEIN TC4; GTPASE, NUCLEAR TRANSPORT, TRANSPORT PROTEIN
1323	1byu	B	27	245	4.8e-33			64.26	GTP-BINDING PROTEIN RAN; CHAIN: A, B;	TRANSPORT PROTEIN TC4; GTPASE, NUCLEAR TRANSPORT, TRANSPORT PROTEIN
1323	1cly	A	31	203	4.8e-64			79.57	RAS-RELATED PROTEIN RAP-1A; CHAIN: A; PROTO-ONKOGENE SERINE/THREONINE PROTEIN KINASE CHAIN: B;	SIGNALING PROTEIN GTP-BINDING PROTEINS, PROTEIN-PROTEIN COMPLEX, EFFECTORS
1323	1eqq	A	33	204	1.3e-64			93.92	TRANSFORMING PROTEIN P21/H-RAS-1; CHAIN: A;	SIGNALING PROTEIN G PROTEIN, GTP HYDROLYSIS, KINETIC CRYSTALLOGRAPHY, 2 SIGNALING PROTEIN
1323	1exz	A	28	204	1.6e-50			52.92	HIS-TAGGED TRANSFORMING PROTEIN RHOA(0-181); CHAIN: A; PKN; CHAIN: B; RAN; CHAIN: A, C; IMPORTIN	SIGNALING PROTEIN PROTEIN-PROTEIN COMPLEX, ANTIPARALLEL COILED-COIL, SMALL GTPASE KARYOPHERIN
1323	1lbr	A	34	209	1.1e-31			60.48		

SEQ NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fsi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1323	1kno		31	204	6.4e-61			91.54	BETA SUBUNIT; CHAIN: B, D; RAP2A; CHAIN: NULL;	BETA, P95 SMALL GTPASE, NUCLEAR TRANSPORT RECEPTOR GTP-BINDING PROTEIN G1P-BINDING PROTEIN, SMALL G PROTEIN, RAP2, GDP, RAS
1323	1mhl		30	222	1.6e-51			62.77	RAC1; CHAIN: NULL;	GTP-BINDING GTP-BINDING, GTP-ASE, SMALL G-PROTEIN, RHO FAMILY, RAS SUPER 2 FAMILY
1323	1rrp	C	31	227	1.1e-31			59.75	RAN; CHAIN: A, C; NUCLEAR PORE COMPLEX PROTEIN NUP358; CHAIN: B, D;	COMPLEX (SMALL GTPASE/NUCLEAR PROTEIN) COMPLEX (SMALL GTPASE/NUCLEAR PROTEIN), SMALL GTPASE, 2 NUCLEAR TRANSPORT
1323	1zbd	A	29	209	9.6e-58			63.61	RAB-3A; CHAIN: A; RABPHILIN-3A; CHAIN: B;	COMPLEX (GTP-BINDING/EFFECTOR) RAS-RELATED PROTEIN RAB3A; COMPLEX (GTP-BINDING/EFFECTOR), G PROTEIN, EFFECTOR, RABCDR, 2 SYNAPTIC EXOCYTOSIS, RAB PROTEIN, RAB3A, RABPHILIN
1323	2ngr	A	33	230	1.6e-46			57.05	GTP BINDING PROTEIN (G25K); CHAIN: A; GTPASE ACTIVATING PROTEIN (RHG); CHAIN: B;	HYDROLASE CDC42/CDC42GAP; CDC42/CDC42GAP; TRANSITION STATE, G-PROTEIN, GAP, CDC42, ALF3, HYDROLASE
1323	3nrb	A	30	204	1.6e-58			67.16	RAB3A; CHAIN: A;	HYDROLASE G PROTEIN, VESICULAR TRAFFICKING, GTP HYDROLYSIS, RAB 2 PROTEIN, NEUROTRANSMITTER RELEASE, HYDROLASE
1324	1a6o		167	536	1.6e-80			107.93	PROTEIN KINASE CK2/ALPHA-SUBUNIT; CHAIN: NULL;	TRANSFERASE TRANSFERASE, SERINE/THREONINE-PROTEIN KINASE, CASEIN KINASE, 2

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fs Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1324	1aq1		196	503	0			129.21	CYCLIN-DEPENDENT PROTEIN KINASE 2; CHAIN: NULL;	SER/THR KINASE PROTEIN KINASE CDK2; PROTEIN KINASE, CELL CYCLE, PHOSPHORYLATION, STAUROSFORMINE, 2 CELL DIVISION, MITOSIS, INHIBITION
1324	1bi8	A	197	493	1.6e-81			122.05	CYCLIN-DEPENDENT KINASE 6; CHAIN: A, C; CYCLIN-DEPENDENT KINASE INHIBITOR; CHAIN: B, D;	COMPLEX (KINASE/INHIBITOR) CDK6; P19INK4D; CYCLIN DEPENDENT KINASE, CYCLIN DEPENDENT KINASE INHIBITORY 2 PROTEIN, CDK, INK4, CELL CYCLE, COMPLEX (KINASE/INHIBITOR) HEADER HELIX
1324	1blx	A	192	499	3.2e-91			133.50	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1324	1cmk	E	160	503	8e-48			102.25	PHOSPHOTRANSFERASE CAMP-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT 1CMK 3 (E.C.2.7.1.37) 1CMK 4	
1324	1ctp	E	165	503	3.2e-47			102.19	TRANSFERASE/PHOSPHOTRANSFERASE) CAMP-DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (CAPK) 1CTP 3 (CATALYTIC SUBUNIT) 1CTP 4	
1324	1bcd		196	503	0			141.09	HUMAN CYCLIN-DEPENDENT KINASE 2; CHAIN: NULL;	PROTEIN KINASE CDK2; TRANSFERASE, SERINE/THREONINE PROTEIN KINASE, ATP-BINDING, 2 CELL CYCLE, CELL DIVISION, MITOSIS, PHOSPHORYLATION

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1324	1lan		180	567	1.6e-97			117.40	P38 MAP KINASE; CHAIN: NULL;	SERINE/THREONINE-PROTEIN KINASE CSBP, R3, P38; PROTEIN SER/THR-KINASE, SERINE/THREONINE-PROTEIN KINASE
1324	1jnk		180	563	9.6e-100			136.35	C-JUN N-TERMINAL KINASE; CHAIN: NULL;	TRANSFERASE JNK3; TRANSFERASE, JNK3 MAP KINASE, SERINE/THREONINE PROTEIN 2 KINASE
1324	1kob	A	170	522	1.6e-51			105.97	TWITCHIN; CHAIN: A, B;	KINASE KINASE, TWITCHIN, INTRASTERIC REGULATION
1324	1p38		179	570	0			150.88	MAP KINASE P38; CHAIN: NULL;	TRANSFERASE MITOGEN ACTIVATED PROTEIN KINASE; TRANSFERASE, MAP KINASE, SERINE/THREONINE-PROTEIN KINASE, 2 P38
1324	1pne		190	568	0			128.64	ERK2; CHAIN: NULL;	TRANSFERASE MAP KINASE, SERINE/THREONINE PROTEIN KINASE, TRANSFERASE
1324	3erk		181	509	0			140.27	EXTRACELLULAR REGULATED KINASE 2; CHAIN: NULL;	TRANSFERASE MITOGEN ACTIVATED PROTEIN KINASE, MAP 2, ERK2; TRANSFERASE, SERINE/THREONINE-PROTEIN KINASE, MAP KINASE, 2 ERK2
1325	1a6o		167	496	6.4e-80			108.11	PROTEIN KINASE CK2/ALPHA-SUBUNIT; CHAIN: NULL;	TRANSFERASE TRANSFERASE, SERINE/THREONINE-PROTEIN KINASE, CASEIN KINASE, 2
1325	1aq1		196	503	0			129.37	CYCLIN-DEPENDENT PROTEIN KINASE 2; CHAIN: NULL;	SER/THR KINASE PROTEIN KINASE CDK2; PROTEIN KINASE, CELL CYCLE, PHOSPHORYLATION, STAUFORFONE, 2 CELL DIVISION, MITOSIS, INHIBITION

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Ψi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1325	1b48	A	197	493	8e-86			122.26	CYCLIN-DEPENDENT KINASE 6; CHAIN: A, C; CYCLIN-DEPENDENT KINASE INHIBITOR; CHAIN: B, D;	COMPLEX (KINASE/INHIBITOR) CDK6; P19INK4D; CYCLIN-DEPENDENT KINASE INHIBITORY 2 PROTEIN, CDK, INK4, CELL CYCLE, COMPLEX (KINASE/INHIBITOR) HEADER HELIX
1325	1b4x	A	192	499	1.3e-94			133.76	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1325	1cmk	E	160	503	3.2e-49			102.41	PHOSPHOTRANSFERASE CAMP-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT 1CMK 3 (E.C.2.7.1.37) 1CMK 4	
1325	1ctp	E	165	503	3.2e-49			102.34	TRANSFERASE (PHOSPHOTRANSFERASE) CAMP-DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (CAPIK) 1CTP 3 (CATALYTIC SUBUNIT) 1CTP 4 (HUMAN CYCLIN-DEPENDENT KINASE 2; CHAIN: NULL;	
1325	1hel		196	503	0			141.19	PROTEIN KINASE CDK2; TRANSFERASE, SERINE/THREONINE PROTEIN KINASE, ATP-BINDING, 2 CELL CYCLE, CELL DIVISION, MITOSIS, PHOSPHORYLATION	
1325	1ham		180	567	0			118.03	P38 MAP KINASE; CHAIN: NULL;	SERINE/THREONINE-PROTEIN KINASE CSBP, RK, P38, PROTEIN SER/THR-KINASE, SERINE/THREONINE-PROTEIN KINASE
1325	1jnk		180	563	4.8e-100			136.46	C-JUN N-TERMINAL KINASE;	TRANSFERASE JNK3;

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOI D score	Compound	PDB annotation
									CHAIN: NULL;	TRANSFERASE, JNK3 MAP KINASE, SERINE/THREONINE PROTEIN 2 KINASE
1325	1lcb	A	170	522	9.6e-53			106.60	TWITCHIN; CHAIN: A, B;	KINASE KINASE, TWITCHIN, INTRASTERIC REGULATION
1325	1p38		179	570	0			151.09	MAP KINASE P38; CHAIN: NULL;	TRANSFERASE MITOGEN ACTIVATED PROTEIN KINASE, TRANSFERASE, MAP KINASE, SERINE/THREONINE-PROTEIN KINASE, 2 P38
1325	1pme		190	568	0			128.85	ERK2; CHAIN: NULL;	TRANSFERASE MAP KINASE, SERINE/THREONINE PROTEIN KINASE, TRANSFERASE
1325	1tki	A	194	519	1.1e-44			99.53	TITIN; CHAIN: A, B;	SERINE KINASE SERINE KINASE, TITIN, MUSCLE, AUTOMYOTON
1325	3erk		181	509	0			140.42	EXTRACELLULAR REGULATED KINASE 2; CHAIN: NULL;	TRANSFERASE MITOGEN ACTIVATED PROTEIN KINASE, MAP 2, ERK2; TRANSFERASE, SERINE/THREONINE-PROTEIN KINASE, MAP KINASE, 2 ERK2
1327	1cs8	A	1	350	0			368.72	HUMAN PROCATHEPSIN L; CHAIN: A;	HYDROLASE PROSEGMENT, PROPEPTIDE, INHIBITION, HYDROLASE
1328	1cs8	A	19	391	0			412.39	HUMAN PROCATHEPSIN L; CHAIN: A;	HYDROLASE PROSEGMENT, PROPEPTIDE, INHIBITION, HYDROLASE
1333	1edh	A	65	269	8e-50			124.30	E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	PstBlast	Verify score	PMF score	SEOFOL D score	Compound	PDB annotation
1333	1ncj	A	64	268	8e-52			129.50	N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN
1335	1adi		3	133	9.6e-56			158.94	LIPID-BINDING PROTEIN ADIPOCYTE LIPID-BINDING PROTEIN COMPLEXED WITH ARACHIDONIC 1ADL 3 ACID 1ADL 4	
1335	1hmr		3	133	6.4e-58			146.24	LIPID-BINDING PROTEIN FATTY ACID BINDING PROTEIN (HUMAN MUSCLE, M-FABP) COMPLEXED 1HMR 3 WITH ONE MOLECULE OF ELAIDIC ACID 1HMR 4	
1335	1pmp	A	3	133	3.2e-55			161.49	CELLULAR LIPOPHILIC TRANSPORT PROTEIN P2 MYELIN PROTEIN (P2) 1PMP 3	
1340	1al2	A	11	409	1.6e-78			141.30	REGULATOR OF CHROMOSOME CONDENSATION 1; CHAIN: A; B; C;	GUANINE NUCLEOTIDE EXCHANGE FACTOR RCC1; GUANINE NUCLEOTIDE EXCHANGE FACTOR, GEF, RAN, 2 RAS-LIKE NUCLEAR GTP BINDING PROTEIN HEADER TER
1345	1e45		1	148	1.4e-61			122.87	GAMMAF CRYSTALLIN; CHAIN: NULL	EYE LENS PROTEIN EYE LENS PROTEIN
1345	1e5d	A	1	148	4.8e-63			121.88	GAMMAE CRYSTALLIN; CHAIN: A, B	EYE LENS PROTEIN EYE LENS PROTEIN
1345	1am		1	148	3.2e-65			125.68	GAMMA B CRYSTALLIN; CHAIN: NULL;	CRYSTALLIN GAMMA II CRYSTALLIN EYE LENS PROTEIN, CRYSTALLIN
1345	1b47	A	1	147	1.6e-39			80.96	CIRCULARLY PERMUTED BB2-CRYSTALLIN; CHAIN: A; B;	EYE-LENS PROTEIN EYE-LENS PROTEIN, BETA-CRYSTALLIN B;

SEQ ID NO:	PDB ID	CHAIN ID	STAR T.AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1345	1elp	A	1	148	1.3e-62			122.84	GAMMA-D CRYSTALLIN; CHAIN: A, B	EYE-LENS PROTEIN, 2 MULTIGENE FAMILY
1345	1gat	B	48	388	9.6e-31			60.77	GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHAIN: G	EYE LENS PROTEIN EYE LENS PROTEIN COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION
1345	2bb2		1	148	1.6e-47			99.58	EYE LENS PROTEIN BETA-B2-CRYSTALLIN 2BB2.3	
1352	2fna		6	177	8e-73			273.99	FERRITIN; CHAIN: NULL;	IRON STORAGE IRON STORAGE
1353	1iqub	A	184	484	1.6e-11			84.05	HUMAN BETA2-GLYCOPROTEIN 1; CHAIN: A;	MEMBRANE ADHESION SHORT CONSENSUS REPEAT, SUSHI, COMPLEMENT CONTROL PROTEIN, 2 N-GLYCOSYLATION, MULTIDOMAIN, MEMBRANE ADHESION
1363	1awc	B	38	192	1.6e-39			64.05	GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABP/ALPHA; GABP/BETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1363	1bd8		2	161	8e-30			54.79	P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1363	1bix	B	1	165	8e-29			55.34	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1363	1bu9	A	31	212	1.6e-34			54.53	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
1363	1lhb	A	5	162	8e-34			54.88	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
1363	1litn	D	73	307	4.8e-38			67.03	NE-KAPPA-B P65 SUBUNIT; CHAIN: A; NE-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKBNFKG COMPLEX
1363	1myo		39	156	3.2e-25			53.66	MYOTROPIN; CHAIN: NULL	ANK-REPEAT MYOTROPIN, ACETYLATION, NMS, ANK-REPEAT
1363	1inf	E	31	243	1.6e-38			64.27	NE-KAPPA-B P65; CHAIN: A, C; NE-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1366	1dqv	A	143	415	8.5e-91	0.64	1.00		SYNAPTOTAGMIN III; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS BETA SANDWICH, CALCIUM ION, C2 DOMAIN
1366	1dqv	A	144	415	3.2e-46	0.49	1.00		SYNAPTOTAGMIN III; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS BETA SANDWICH, CALCIUM ION, C2 DOMAIN

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1366	Irsy		134	270	3.4e-40	0.40	1.00		CALCIUM/PHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN I (FIRST C2 DOMAIN) (CALB) IRSY 3	
1366	Irsy		134	270	3.4e-40			122.64	CALCIUM/PHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN I (FIRST C2 DOMAIN) (CALB) IRSY 3	
1368	1bu7	A	42	505	1.6e-92			197.06	CYTCHROME P450; CHAIN: A, B;	OXIDOREDUCTASE FATTY ACID HYDROXYLASE; FATTY ACID MONOOXYGENASE, HEMOPROTEIN, P450 REMARK
1368	1oxa		23	504	3.2e-31			67.59	CYTCHROME P450 ERYF: 10XA 5 CHAIN: NULL, 10XA 6	OXIDOREDUCTASE (OXYGENASE)
1372	1bg2		2	340	8e-89			210.20	KINESIN; CHAIN: NULL;	MOTOR PROTEIN MOTOR PROTEIN, ATPASE, MICROTUBULE ASSOCIATED
1372	1bg2		4	340	8e-89	0.54	1.00		KINESIN; CHAIN: NULL;	MOTOR PROTEIN MOTOR PROTEIN, ATPASE, MICROTUBULE ASSOCIATED
1372	1ez7	A	1	340	6.8e-79	0.65	1.00		MICROTUBULE MOTOR PROTEIN NCD; CHAIN: A, B, C, D;	CONTRACTILE PROTEIN NCD, CLARET SEGREGATIONAL PROTEIN; NCD CRYSTAL STRUCTURE, MICROTUBULE MOTORS, KINESIN 2 SUPERFAMILY, CONTRACTILE PROTEIN
1372	1ez7	A	1	341	3.2e-72	0.46	1.00		MICROTUBULE MOTOR PROTEIN NCD; CHAIN: A, B, C, D;	CONTRACTILE PROTEIN NCD, CLARET SEGREGATIONAL PROTEIN; NCD CRYSTAL STRUCTURE, MICROTUBULE MOTORS, KINESIN 2 SUPERFAMILY, CONTRACTILE PROTEIN

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Bias	Verify score	PMF score	SEQOL D score	Compound	PDB annotation
1372	1ez7	A	1	342	6.8e-79			156.19	MICROTUBULE MOTOR PROTEIN NCD; CHAIN: A, B, C, D;	CONTRACTILE PROTEIN NCD, CLARET SEGREGATIONAL PROTEIN; NCD CRYSTAL STRUCTURE, MICROTUBULE MOTORS, KINESIN 2 SUPERFAMILY, CONTRACTILE PROTEIN
1372	2kin	A	2	252	1.2e-58			139.58	KINESIN; CHAIN: A, B;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
1372	2kin	A	4	252	3.2e-57	0.25	1.00		KINESIN; CHAIN: A, B;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
1372	2kin	A	6	252	1.2e-58	0.29	1.00		KINESIN; CHAIN: A, B;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
1372	2kin	B	265	352	3.4e-28	-0.01	0.98		KINESIN; CHAIN: A, B;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
1372	2kin	B	265	358	8e-27	-0.02	0.99		KINESIN; CHAIN: A, B;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
1372	2ned	A	1	339	1.6e-72	0.46	1.00		KINESIN MOTOR NCD; CHAIN: A;	CONTRACTILE PROTEIN KINESIN, MICROTUBULE-BASED MOTOR, NCD, CONTRACTILE PROTEIN
1372	2ned	A	1	340	1.6e-72			152.53	KINESIN MOTOR NCD; CHAIN: A;	CONTRACTILE PROTEIN KINESIN, MICROTUBULE-BASED MOTOR, NCD, CONTRACTILE PROTEIN
1372	3kar		5	338	5.1e-74			185.05	KINESIN-LIKE PROTEIN KAR3; CHAIN: NULL;	CONTRACTILE PROTEIN KINESIN, KINESIN-RELATED PROTEIN, MOTOR 2 PROTEIN, ATPASE, P-LOOP, MICROTUBULE BINDING PROTEIN
1372	3kar		6	339	6.4e-72	0.31	1.00		KINESIN-LIKE PROTEIN KAR3; CHAIN: NULL;	CONTRACTILE PROTEIN KINESIN, KINESIN-RELATED PROTEIN, MOTOR 2 PROTEIN, ATPASE, P-LOOP, MICROTUBULE BINDING PROTEIN

SEQ NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
1372	3kar		7	338	5.1e-74	0.50	1.00		KINESIN-LIKE PROTEIN KAR3; CHAIN: NULL;	CONTRACTILE PROTEIN, KAR3, KINESIN-RELATED PROTEIN, MOTOR 2 PROTEIN, ATPASE, P-LOOP, MICROTUBULE BINDING PROTEIN
1372	3kin	B	269	352	1.4e-26	0.19	0.99		KINESIN HEAVY CHAIN; CHAIN: A, B, C, D;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
1372	3kin	B	269	384	3.2e-26	-0.10	0.98		KINESIN HEAVY CHAIN; CHAIN: A, B, C, D;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
1373	1a4y	A	123	448	4.8e-12	0.19	0.04		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPTOPE MAPPING, LEUCINE-RICH 3 REPEATS
1373	1a4y	A	134	545	4.8e-09	0.26	-0.05		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPTOPE MAPPING, LEUCINE-RICH 3 REPEATS
1373	1a4y	A	45	361	9.6e-14	0.10	0.00		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPTOPE MAPPING, LEUCINE-RICH 3 REPEATS
1373	1a4y	A	63	230	1e-19	0.29	0.37		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPTOPE MAPPING, LEUCINE-RICH 3 REPEATS

SEQ ID NO:	PDB ID	CHAIN ID	STAR T.AA	END AA	Psi Binst	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1373	1a9n	A	114	264	5.1e-19	0.66	0.42		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A; CHAIN: A, C; U2 B; CHAIN: B, D;	3 REPEATS COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP RIBONUCLEOPROTEIN
1373	1a9n	A	65	220	3.4e-22	0.43	0.17		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A; CHAIN: A, C; U2 B; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP RIBONUCLEOPROTEIN
1373	1a9n	A	90	231	3.4e-19	0.55	0.65		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A; CHAIN: A, C; U2 B; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP RIBONUCLEOPROTEIN
1373	1a9n	C	114	264	3.4e-18	0.48	0.53		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A; CHAIN: A, C; U2 B; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP RIBONUCLEOPROTEIN
1373	1a9n	C	65	220	1.4e-22	0.24	0.04		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A; CHAIN: A, C; U2 B; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP RIBONUCLEOPROTEIN
1373	1a9n	C	90	231	3.4e-19	0.66	0.55		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A; CHAIN: A, C; U2 B; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP RIBONUCLEOPROTEIN
1373	1b1h	A	294	367	6.8e-14	0.33	0.77		HEMOLIN; CHAIN: A, B;	INSECT IMMUNITY INSECT IMMUNITY, 1PS-BINDING, HOMOPHILIC ADHESION
1373	1b1h	A	295	427	1.7e-10	0.37	0.25		HEMOLIN; CHAIN: A, B;	INSECT IMMUNITY INSECT IMMUNITY, 1PS-BINDING, HOMOPHILIC ADHESION
1373	1b1v		421	506	3.4e-07	-0.04	0.07		TITIN; CHAIN: NULL;	CONNECTIN A71, CONNECTIN; TITIN, CONNECTIN, FIBRONECTIN TYPE III

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1373	1c56	A	286	388	8.5e-15	0.01	-0.05		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
1373	1c56	A	295	409	3.4e-12	0.31	0.19		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
1373	1c5s	C	306	389	8.5e-14	0.65	1.00		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR GROWTH FACTOR RECEPTOR
1373	1c5s	D	296	383	1.2e-14	0.29	0.57		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR GROWTH FACTOR RECEPTOR
1373	1d0b	A	152	310	6.4e-26	0.02	0.05		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1373	1d0b	A	176	332	8e-24	0.09	-0.15		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1373	1d0b	A	37	211	1.4e-22	0.13	0.57		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1373	1d0b	A	423	547	1.6e-14	0.05	-0.19		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1373	1d0b	A	79	265	8e-22	0.31	0.30		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1373	1dce	A	32	95	9.6e-09	-0.43	0.23		RAB GERANYLGERANYLTRANSFERASE ALPHA SUBUNIT;	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									CHAIN: A, C, RAB GERANYLGERANYLTRANSFERASE BETA SUBUNIT; CHAIN: B, D;	2.0 Å 2 RESOLUTION, N-FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
1373	1de2	A	37	171	8e-08	-0.03	0.15		RAB GERANYLGERANYLTRANSFERASE ALPHA SUBUNIT; CHAIN: A, C, RAB GERANYLGERANYLTRANSFERASE BETA SUBUNIT; CHAIN: B, D;	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 Å 2 RESOLUTION, N-FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
1373	1ds9	A	56	186	1.6e-10	-0.41	0.28		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE-RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS FLAGELLA
1373	1ev2	E	292	383	5.1e-14	0.13	-0.08		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGFR2; FGFR2; IMMUNOGLOBULIN (IG)-LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, 3-TREFOIL FOLD
1373	1ev2	G	296	387	6.8e-16	0.22	0.13		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGFR2; FGFR2; IMMUNOGLOBULIN (IG)-LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, 3-TREFOIL FOLD
1373	1fw	A	64	231	1.7e-13	0.26	0.54		SKP2; CHAIN: A, C, E, G, I, K, M, O; SKP1; CHAIN: B, D, F, H, J, L, N, P;	LIGASE CYCLIN A/CDC2-ASSOCIATED PROTEIN P45; CYCLIN A/CDC2-ASSOCIATED PROTEIN P19; SKP1, SKP2, F-BOX, 1.8 Å, LEUCINE-RICH REPEAT, SCP, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE
1373	1fs2	A	53	231	3.4e-18	0.03	0.31		SKP2; CHAIN: A, C, SKP1;	LIGASE CYCLIN A/CDC2-

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									CHAIN: B, D;	ASSOCIATED P45; CYCLIN A/CDK2-ASSOCIATED P19; SKP1, SKP2, F-box, LRRs, LEUCINE-RICH REPEATS, SCP, 2 UBIQUITIN, E3, UBIQUITIN PROTEIN LIGASE
1373	1huf		303	405	1.7e-08	0.39	0.27		1 LYMPHOCYTE ADHESION GLYCOPROTEIN CD2 (HUMAN) 1HNF 3	
1373	1net		292	383	6.8e-19	0.56	0.31		TITIN; CHAIN: NULL;	MUSCLE PROTEIN CONNECTIN, NEXTIN5; CELL ADHESION, GLYCOPROTEIN, TRANSMEMBRANE, REPEAT, BRAIN, 2 IMMUNOGLOBULIN FOLD, ALTERNATIVE SPLICING, SIGNAL, 3 MUSCLE PROTEIN
1373	1nm		305	383	1.7e-16	0.60	0.76		MUSCLE PROTEIN TITIN MODULE M5 (CONNECTIN) 1TNM 3 (NMR, MINIMIZED AVERAGE STRUCTURE) 1TNM 4 1TNM 58	
1373	1ntf		424	502	3.4e-07	-0.29	0.40		GLYCOPROTEIN FIBRONECTIN (TENTH TYPE III MODULE) (NMR, 36 STRUCTURES) ITTF 3	
1373	1vea	A	297	394	1.7e-11	0.46	0.16		HUMAN VASCULAR CELL ADHESION MOLECULE-1; 1VCA 4 CHAIN: A, B; 1VCA 5	CELL ADHESION PROTEIN VCAM-DI.2; 1VCA 6 IMMUNOGLOBULIN SUPERFAMILY, INTEGRIN-BINDING 1VCA 15
1373	1wio	A	280	411	3.4e-12	0.37	0.00		T-CELL SURFACE GLYCOPROTEIN CD4; CHAIN: A, B;	GLYCOPROTEIN CD4; IMMUNOGLOBULIN FOLD, TRANSMEMBRANE, GLYCOPROTEIN, T-CELL, 2 MHC LIPOPROTEIN, POLYMORPHISM
1373	1yrg	A	132	362	1.1e-09	0.04	-0.14		GTPASE-ACTIVATING PROTEIN RNAI SCHPO;	TRANSCRIPTION RNAI; RANGAP; GTPASE-ACTIVATING PROTEIN

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									CHAIN: A, B;	FOR SPI1, GTPASE-ACTIVATING PROTEIN GAP, RNAIP, RANGAP, LRR, LEUCINE-2 RICH REPEAT PROTEIN, TWINNING, HEMISPHERAL TWINNING, 3 MEROPEDRAL TWINNING, MEROPEDRY
1373	2bnh		45	359	1.4e-18	0.04	0.03		RIBONUCLEASE INHIBITOR; CHAIN: NULL;	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS
1373	2bnh		47	231	1.7e-23	0.13	0.06		RIBONUCLEASE INHIBITOR; CHAIN: NULL;	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS
1373	2dji	A	294	396	3.4e-11	0.20	-0.05		MHC CLASS I NK CELL RECEPTOR PRECURSOR; CHAIN: A;	IMMUNE SYSTEM P58 NATURAL KILLER CELL RECEPTOR, NATURAL KILLER RECEPTOR, INHIBITORY RECEPTOR, 2 IMMUNOGLOBULIN
1373	3ncm	A	296	383	3.4e-17	0.92	0.35		NEURAL CELL ADHESION MOLECULE, LARGE ISOFORM; CHAIN: A;	CELL ADHESION PROTEIN NCAM MODULE 2; CELL ADHESION, GLYCOPROTEIN, HEPARIN-BINDING, GPI-ANCHOR, 2 NEURAL ADHESION MOLECULE, IMMUNOGLOBULIN FOLD, HOMOPHILIC 3 BINDING, CELL ADHESION PROTEIN
1374	1cmu	A	65	293	0.0017			61.31	ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1374	1ez7	A	1	131	5.1e-34	-0.46	0.66		MICROTUBULE MOTOR PROTEIN NCD; CHAIN: A, B, C, D;	CONTRACTILE PROTEIN NCD, CLARET SEGREGATIONAL PROTEIN; NCD CRYSTAL STRUCTURE, MICROTUBULE MOTORS, KINESIN 2 SUPERFAMILY, CONTRACTILE PROTEIN
1374	1quu	A	53	295	3.4e-05			66.44	HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL, CONTRACTILE PROTEIN
1374	1sig		36	318	0.0017			65.31	RNA POLYMERASE PRIMARY SIGMA FACTOR; CHAIN: NULL;	TRANSCRIPTION REGULATION SIGMA70; RNA POLYMERASE SIGMA FACTOR, TRANSCRIPTION REGULATION
1374	2kin	A	1	42	5.1e-15	-0.55	0.12		KINESIN; CHAIN: A, B;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
1374	2kin	B	55	141	1.7e-27	-0.41	0.81		KINESIN; CHAIN: A, B;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
1374	2kin	B	55	154	1.7e-27			65.43	KINESIN; CHAIN: A, B;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
1374	3kar		1	127	1e-30	-0.52	0.60		KINESIN-LIKE PROTEIN KAR3; CHAIN: NULL;	CONTRACTILE PROTEIN CONTRACTILE PROTEIN, KAR3, KINESIN-RELATED PROTEIN, MOTOR 2 PROTEIN, ATPASE, P-LOOP, MICROTUBULE BINDING PROTEIN
1374	3kin	B	59	142	6.8e-25	-0.15	0.86		KINESIN HEAVY CHAIN; CHAIN: A, B, C, D;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
1374	3kin	B	59	176	6.8e-25			68.48	KINESIN HEAVY CHAIN; CHAIN: A, B, C, D;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
1376	1eej	A	323	405	5.1e-19	-0.02	0.03		MEROZOITE SURFACE PROTEIN 1; CHAIN: A;	SURFACE PROTEIN MEROZOITE SURFACE ANTIGEN 1, MAJOR BLOOD-STAGE EGF-LIKE DOMAIN, EXTRACELLULAR, MODULAR

SEQ NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										PROTEIN, SURFACE 2 ANTIGEN, MALARIA VACCINE COMPONENT, SURFACE PROTEIN
1376	1cej	A	364	435	6.8e-17	-0.11	0.41		MEROZOITE SURFACE PROTEIN 1; CHAIN: A;	SURFACE PROTEIN MEROZOITE SURFACE ANTIGEN 1, MAJOR BLOOD-STAGE EGF-LIKE DOMAIN, EXTRACELLULAR, MODULAR PROTEIN, SURFACE 2 ANTIGEN, MALARIA VACCINE COMPONENT, SURFACE PROTEIN
1376	1cej	A	403	481	5.1e-09	0.08	-0.14		MEROZOITE SURFACE PROTEIN 1; CHAIN: A;	SURFACE PROTEIN MEROZOITE SURFACE ANTIGEN 1, MAJOR BLOOD-STAGE EGF-LIKE DOMAIN, EXTRACELLULAR, MODULAR PROTEIN, SURFACE 2 ANTIGEN, MALARIA VACCINE COMPONENT, SURFACE PROTEIN
1376	1cej	A	45	128	5.1e-21	0.09	0.53		MEROZOITE SURFACE PROTEIN 1; CHAIN: A;	SURFACE PROTEIN MEROZOITE SURFACE ANTIGEN 1, MAJOR BLOOD-STAGE EGF-LIKE DOMAIN, EXTRACELLULAR, MODULAR PROTEIN, SURFACE 2 ANTIGEN, MALARIA VACCINE COMPONENT, SURFACE PROTEIN
1376	1d4v	A	631	733	1.4e-08	0.30	-0.13		TNF-RELATED APOPTOSIS INDUCING LIGAND; CHAIN: B; DEATH RECEPTOR 5; CHAIN: A;	APOPTOSIS TRAIL; DR5; LIGAND-RECEPTOR COMPLEX, TRIMERIC JELLY-ROLL, TNF-R 2 SUPERFAMILY, APOPTOSIS
1376	1d4b	A	181	252	5.1e-14	0.76	0.78		THROMBOMODULIN; CHAIN: A;	MEMBRANE PROTEIN NMR, THROMBIN, EGF MODULE, ANTICOAGULANT, GLYCOSYLATION
1376	1d4b	A	321	406	5.1e-18	0.30	0.15		THROMBOMODULIN; CHAIN: A;	MEMBRANE PROTEIN NMR, THROMBIN, EGF MODULE,

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1376	1dqb	A	400	485	5.1e-10	-0.07	0.00		THROMBOMODULIN; CHAIN: A;	ANTICOAGULANT, GLYCOSYLATION
1376	1dqb	A	44	131	5.1e-18	0.25	0.21		THROMBOMODULIN; CHAIN: A;	MEMBRANE PROTEIN NMR, THROMBIN, EGF MODULE, ANTICOAGULANT, GLYCOSYLATION
1376	1edim	B	403	433	3.4e-07	-0.14	0.23		FACTOR IX; CHAIN: B, C;	MEMBRANE PROTEIN NMR, THROMBIN, EGF MODULE, ANTICOAGULANT, GLYCOSYLATION
										COAGULATION FACTOR CRYSTAL STRUCTURE, EPIDERMAL GROWTH FACTOR, EGF, 2 CALCIUM-BINDING, EGF-LIKE DOMAIN, STRUCTURE AND FUNCTION, 3 HUMAN FACTOR IX, COAGULATION FACTOR
1376	1f7e	A	403	433	5.1e-07	0.09	0.04		BLOOD COAGULATION FACTOR VII; CHAIN: A;	BLOOD CLOTTING FACTOR VII, BLOOD COAGULATION, EGF-LIKE DOMAIN, BLOOD 2 CLOTTING
1376	1fjs	L	216	254	1.2e-12	0.66	0.23		COAGULATION FACTOR XA; CHAIN: A; COAGULATION FACTOR XA; CHAIN: L;	BLOOD CLOTTING PROTEIN INHIBITOR COMPLEX, COAGULATION COFACTOR, PROTEASE
1376	1fjs	L	284	335	3.4e-20	0.27	0.42		COAGULATION FACTOR XA; CHAIN: A; COAGULATION FACTOR XA; CHAIN: L;	BLOOD CLOTTING PROTEIN INHIBITOR COMPLEX, COAGULATION COFACTOR, PROTEASE
1376	1fjs	L	327	374	1.7e-17	-0.13	0.25		COAGULATION FACTOR XA; CHAIN: A; COAGULATION FACTOR XA; CHAIN: L;	BLOOD CLOTTING PROTEIN INHIBITOR COMPLEX, COAGULATION COFACTOR, PROTEASE
1376	1fjs	L	407	445	1.4e-15	0.08	0.94		COAGULATION FACTOR XA; CHAIN: A; COAGULATION	BLOOD CLOTTING PROTEIN INHIBITOR COMPLEX,

SEQ ID NO:	PDB ID	CHAI ID	STAR T AA	END AA	Fsi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1376	1lfs	L	49	90	1.7e-12	0.83	0.59		FACTOR XA; CHAIN: L; COAGULATION FACTOR XA; CHAIN: A; COAGULATION FACTOR XA; CHAIN: L;	COAGULATION COFACTOR, PROTEASE BLOOD CLOTTING PROTEIN INHIBITOR COMPLEX, COAGULATION COFACTOR, PROTEASE
1376	1hcg	B	217	254	3.4e-12	0.50	0.46		COAGULATION FACTOR BLOOD COAGULATION FACTOR XA IHCG 3	
1376	1hcg	B	286	334	1.2e-18	0.34	0.33		COAGULATION FACTOR BLOOD COAGULATION FACTOR XA IHCG 3	
1376	1hcg	B	407	445	8.5e-15	0.45	0.89		COAGULATION FACTOR BLOOD COAGULATION FACTOR XA IHCG 3	
1376	1hcg	B	49	90	5.1e-12	0.45	0.95		COAGULATION FACTOR BLOOD COAGULATION FACTOR XA IHCG 3	
1376	1lkg	L	327	374	3.4e-18	0.01	0.31		FACTOR XA; CHAIN: H, L; ANTICOAGULANT PEPTIDE; CHAIN: I;	COMPLEX (PROTEASE/INHIBITOR) RTAP; GLYCOPROTEIN, SERINE PROTEASE, PLASMA, BLOOD COAGULATION, 2 COMPLEX (PROTEASE/INHIBITOR)
1376	1lkg	L	407	445	6.8e-15	-0.06	0.82		FACTOR XA; CHAIN: H, L; ANTICOAGULANT PEPTIDE; CHAIN: I;	COMPLEX (PROTEASE/INHIBITOR) RTAP; GLYCOPROTEIN, SERINE PROTEASE, PLASMA, BLOOD COAGULATION, 2 COMPLEX (PROTEASE/INHIBITOR)
1376	1lkg	L	49	90	5.1e-12	0.66	0.34		FACTOR XA; CHAIN: H, L; ANTICOAGULANT PEPTIDE; CHAIN: I;	COMPLEX (PROTEASE/INHIBITOR) RTAP; GLYCOPROTEIN, SERINE PROTEASE, PLASMA, BLOOD COAGULATION, 2 COMPLEX (PROTEASE/INHIBITOR)
1376	1lko		135	322	6.8e-14	0.47	-0.11		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Fsi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1376	1kfo		286	433	1.7e-20	0.16	-0.18		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
1376	1kfo		626	787	8.5e-10	0.38	0.00		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
1376	1pfx	L	121	254	1.7e-14	0.04	0.01		FACTOR IXA; CHAIN: C, L, D; PHE-PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM- BINDING, HYDROLASE, 3 GLYCOPROTEIN
1376	1pfx	L	289	427	3.4e-27	0.02	0.23		FACTOR IXA; CHAIN: C, L, D; PHE-PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM- BINDING, HYDROLASE, 3 GLYCOPROTEIN
1376	1pfx	L	41	152	8.5e-26	0.21	0.89		FACTOR IXA; CHAIN: C, L, D; PHE-PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM- BINDING, HYDROLASE, 3 GLYCOPROTEIN
1376	1qtk	L	131	226	1.4e-22	0.28	0.37		COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRYPTEPTIDYL INHIBITOR; CHAIN: C;	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE
1376	1qtk	L	177	232	8.5e-16	0.18	0.72		COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L;	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	F ₅₀ Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	PROTEASE
1376	1qtk	L	286	389	3.4e-26	-0.11	0.22		COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE
1376	1qtk	L	326	419	1.5e-21	-0.01	0.29		COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE
1376	1qtk	L	367	445	1e-18	0.22	0.99		COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE
1376	1qtk	L	48	141	1.7e-24	0.12	0.92		COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE
1376	1qtk	L	89	189	6.8e-23	-0.29	0.52		COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE

SEQ NO.	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1376	Iqub	A	41	444	1.7e-46	0.02	-0.18		HUMAN BETA2-GLYCOPROTEIN I; CHAIN: A;	MEMBRANE ADHESION SHORT CONSENSUS REPEAT, SUSHI, COMPLEMENT CONTROL PROTEIN, 2 N-GLYCOSYLATION, MULTIDOMAIN MEMBRANE ADHESION
1376	Irfn	B	175	228	1e-13	0.24	0.35		COAGULATION FACTOR IX; CHAIN: A; COAGULATION FACTOR IX; CHAIN: B;	COAGULATION FACTOR SERINE PROTEINASE, BLOOD COAGULATION, COAGULATION FACTOR
1376	Irfn	B	285	339	3.4e-19	0.29	-0.01		COAGULATION FACTOR IX; CHAIN: A; COAGULATION FACTOR IX; CHAIN: B;	COAGULATION FACTOR SERINE PROTEINASE, BLOOD COAGULATION, COAGULATION FACTOR
1376	Irfn	B	407	445	3.4e-11	0.13	0.94		COAGULATION FACTOR IX; CHAIN: A; COAGULATION FACTOR IX; CHAIN: B;	COAGULATION FACTOR SERINE PROTEINASE, BLOOD COAGULATION, COAGULATION FACTOR
1376	Irfn	B	49	102	8.5e-12	0.67	-0.15		COAGULATION FACTOR IX; CHAIN: A; COAGULATION FACTOR IX; CHAIN: B;	COAGULATION FACTOR SERINE PROTEINASE, BLOOD COAGULATION, COAGULATION FACTOR
1376	Isp		805	918	3.4e-21	0.64	0.48		ASFP; CHAIN: NULL;	SPERMADHESIN ACIDIC SEMINAL PROTEIN; SPERMADHESIN, BOVINE SEMINAL PLASMA PROTEIN, ACIDIC 2 SEMINAL FLUID PROTEIN, ASFP, CUB DOMAIN, X-RAY CRYSTAL 3 STRUCTURE, GROWTH FACTOR
1376	Isp	B	809	922	3.4e-22	0.37	0.65		MAJOR SEMINAL PLASMA GLYCOPROTEIN PSP-II; CHAIN: A; MAJOR SEMINAL PLASMA GLYCOPROTEIN PSP-II; CHAIN: B	COMPLEX SEMINAL PLASMA PROTEIN(SPP) SEMINAL PLASMA PROTEINS, SPERMADHESIN, CUB DOMAIN 2 ARCHITECTURE, COMPLEX (SEMINAL PLASMA PROTEIN(SPP))

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1376	1lpg		68	158	1.5e-21	0.05	0.04		T-PLASMINOGEN ACTIVATOR FI-G; 1TPG 7 CHAIN: NULL; 1TPG 8	PLASMINOGEN ACTIVATION
1376	1xka	L	131	230	1.7e-15	0.09	0.59		BLOOD COAGULATION FACTOR XA; CHAIN: L; C;	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN
1376	1xka	L	182	254	1.7e-15	-0.01	0.43		BLOOD COAGULATION FACTOR XA; CHAIN: L; C;	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN
1376	1xka	L	286	380	5.1e-20	0.25	0.69		BLOOD COAGULATION FACTOR XA; CHAIN: L; C;	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN
1376	1xka	L	367	444	3.4e-19	0.28	0.40		BLOOD COAGULATION FACTOR XA; CHAIN: L; C;	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN
1376	1xka	L	48	145	3.4e-22	0.01	0.55		BLOOD COAGULATION FACTOR XA; CHAIN: L; C;	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN
1381	1a06		205	530	5.1e-62	-0.04	0.71		CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE; CHAIN: NULL;	KINASE KINASE, SIGNAL TRANSDUCTION, CALCIUM/CALMODULIN
1381	1a06		256	534	5.1e-62			109.19	CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE;	KINASE KINASE, SIGNAL TRANSDUCTION,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psj Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1381	1hel		202	495	1.7e-53	0.39	1.00		(CATALYTIC SUBUNIT) ICTP 4. HUMAN CYCLIN-DEPENDENT KINASE 2; CHAIN: NULL;	PROTEIN KINASE CDK2; TRANSFERASE, SERINE/THREONINE PROTEIN KINASE, ATP-BINDING, 2 CELL CYCLE, CELL DIVISION, MITOSIS, PHOSPHORYLATION
1381	1hel		202	499	1.7e-53			115.78	HUMAN CYCLIN-DEPENDENT KINASE 2; CHAIN: NULL;	PROTEIN KINASE CDK2; TRANSFERASE, SERINE/THREONINE PROTEIN KINASE, ATP-BINDING, 2 CELL CYCLE, CELL DIVISION, MITOSIS, PHOSPHORYLATION
1381	1ian		183	555	3.4e-40			92.87	P38 MAP KINASE; CHAIN: NULL;	SERINE/THREONINE-PROTEIN KINASE CSBP, RK, P38; PROTEIN SER/THR-KINASE, SERINE/THREONINE-PROTEIN KINASE
1381	1ian		203	475	3.4e-40	0.01	0.88		P38 MAP KINASE; CHAIN: NULL;	SERINE/THREONINE-PROTEIN KINASE CSBP, RK, P38; PROTEIN SER/THR-KINASE, SERINE/THREONINE-PROTEIN KINASE
1381	1jnk		185	577	1.7e-46			112.39	C-JUN N-TERMINAL KINASE; CHAIN: NULL;	TRANSFERASE JNK3; TRANSFERASE, JNK3 MAP KINASE, SERINE/THREONINE PROTEIN 2 KINASE
1381	1jnk		203	512	1.7e-46	0.21	1.00		C-JUN N-TERMINAL KINASE; CHAIN: NULL;	TRANSFERASE JNK3; TRANSFERASE, JNK3 MAP KINASE, SERINE/THREONINE PROTEIN 2 KINASE
1381	1kcb	A	170	570	1.7e-68			127.80	TWITCHIN; CHAIN: A, B;	KINASE KINASE, TWITCHIN, INTRASTERIC REGULATION
1381	1kcb	A	205	493	1.7e-68	0.32	1.00		TWITCHIN; CHAIN: A, B;	KINASE KINASE, TWITCHIN,

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1381	3erk		198	498	8.5e-53	0.54	1.00		EXTRACELLULAR REGULATED KINASE 2; CHAIN: NULL;	INTRASTERIC REGULATION TRANSFERASE MITOGEN ACTIVATED PROTEIN KINASE, MAP 2, ERK2; TRANSFERASE, SERINE/THREONINE-PROTEIN KINASE, MAP KINASE, 2 ERK2
1381	3erk		213	562	8.5e-53			98.67	EXTRACELLULAR REGULATED KINASE 2; CHAIN: NULL;	TRANSFERASE MITOGEN ACTIVATED PROTEIN KINASE, MAP 2, ERK2; TRANSFERASE, SERINE/THREONINE-PROTEIN KINASE, MAP KINASE, 2 ERK2
1384	1ao7	E	52	210	9.6e-54	0.39	1.00		HLA-A 0201; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; TAX PEPTIDE; CHAIN: C; T CELL RECEPTOR ALPHA; CHAIN: D; T CELL RECEPTOR BETA; CHAIN: E;	COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR) HLA-A2 HEAVY CHAIN; CLASS I MHC, T-CELL RECEPTOR, VIRAL PEPTIDE, 2 COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR)
1384	1ao7	E	52	210	9.6e-54			128.38	HLA-A 0201; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; TAX PEPTIDE; CHAIN: C; T CELL RECEPTOR ALPHA; CHAIN: D; T CELL RECEPTOR BETA; CHAIN: E;	COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR) HLA-A2 HEAVY CHAIN; CLASS I MHC, T-CELL RECEPTOR, VIRAL PEPTIDE, 2 COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR)
1384	1bd2	E	52	210	3.2e-66	0.48	1.00		HLA-A 0201; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; TAX PEPTIDE; CHAIN: C; T CELL RECEPTOR ALPHA; CHAIN: D; T CELL RECEPTOR BETA; CHAIN: E;	COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR) HLA A2 HEAVY CHAIN; COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR)
1384	1bd2	E	52	210	3.2e-66			143.49	HLA-A 0201; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; TAX PEPTIDE; CHAIN: C; T CELL RECEPTOR ALPHA;	COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR) HLA A2 HEAVY CHAIN; COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR)

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1384	1bec		52	210	6.4e-66			130.56	CHAIN: D; T CELL RECEPTOR BETA; CHAIN: E; 14.3.D T CELL ANTIGEN RECEPTOR; IBE5 5 CHAIN; NULL; IBE6 6	RECEPTOR T CELL RECEPTOR IBE5 14
1384	1bec		53	210	6.4e-66	0.49	1.00		14.3.D T CELL ANTIGEN RECEPTOR; IBE5 5 CHAIN; NULL; IBE6 6	RECEPTOR T CELL RECEPTOR IBE5 14
1384	1f54	E	53	210	8e-60	0.25	1.00		HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR CHAIN: A; HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-1 CHAIN: B; HEMAGGLUTININ HAI PEPTIDE CHAIN; CHAIN: C; T-CELL RECEPTOR ALPHA CHAIN; CHAIN: D; T-CELL RECEPTOR BETA CHAIN; CHAIN: E;	IMMUNE SYSTEM HLA-DRI, DRA; HLA-DRI, DRB1 0101; TCR HAI.7 ALPHA CHAIN; TCR HAI.7 BETA CHAIN; PROTEIN-PROTEIN COMPLEX, IMMUNOGLOBULIN FOLD
1384	1ter	B	50	210	9.6e-64	0.43	1.00		ALPHA, BETA T-CELL RECEPTOR CHAIN: A, B;	RECEPTOR TCR; T-CELL, RECEPTOR, TRANSMEMBRANE, GLYCOPROTEIN, SIGNAL
1384	1ter	B	51	210	9.6e-64			131.76	ALPHA, BETA T-CELL RECEPTOR CHAIN: A, B;	RECEPTOR TCR; T-CELL, RECEPTOR, TRANSMEMBRANE, GLYCOPROTEIN, SIGNAL
1388	1a4y	A	21	309	3.2e-17	0.04	-0.11		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPTOPE MAPPING, LEUCINE-RICH 3 REPEATS
1388	1a6n	A	26	156	3.4e-21	0.43	-0.01		U2 RNA HAIRPIN IV; CHAIN: Q;	COMPLEX (NUCLEAR

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									R; U2 A'; CHAIN: A, C; U2 B'; CHAIN: B, D;	PROTEIN(RNA) COMPLEX (NUCLEAR PROTEIN(RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1388	1a9n	A	46	155	4.8e-06	0.28	0.19		U2 RNA HAIRPIN IV; CHAIN: Q; R; U2 A'; CHAIN: A, C; U2 B'; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN(RNA) COMPLEX (NUCLEAR PROTEIN(RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1388	1a9n	A	4	121	1.5e-20	0.48	0.65		U2 RNA HAIRPIN IV; CHAIN: Q; R; U2 A'; CHAIN: A, C; U2 B'; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN(RNA) COMPLEX (NUCLEAR PROTEIN(RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1388	1a9n	C	24	106	1.3e-05	0.51	0.51		U2 RNA HAIRPIN IV; CHAIN: Q; R; U2 A'; CHAIN: A, C; U2 B'; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN(RNA) COMPLEX (NUCLEAR PROTEIN(RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1388	1a9n	C	26	156	1.2e-21	0.41	-0.08		U2 RNA HAIRPIN IV; CHAIN: Q; R; U2 A'; CHAIN: A, C; U2 B'; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN(RNA) COMPLEX (NUCLEAR PROTEIN(RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1388	1a9n	C	46	155	4.8e-06	0.42	0.06		U2 RNA HAIRPIN IV; CHAIN: Q; R; U2 A'; CHAIN: A, C; U2 B'; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN(RNA) COMPLEX (NUCLEAR PROTEIN(RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1388	1a9n	C	4	121	6.8e-20	0.67	0.89		U2 RNA HAIRPIN IV; CHAIN: Q; R; U2 A'; CHAIN: A, C; U2 B'; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN(RNA) COMPLEX (NUCLEAR PROTEIN(RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1388	1a66	A	77	280	0.00034	-0.15	0.07		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL
1388	1d0b	A	19	194	6.4e-27	0.50	0.77		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT; CALCIUM BINDING, CELL
1388	1d0b	A	4	128	1.4e-12	0.27	0.89		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT; CALCIUM BINDING, CELL

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1388	1d0b	A	63	216	1.4e-25	0.28	0.43		INTERNALIN B; CHAIN: A;	ADHESION CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1388	1d0b	A	87	236	3.2e-25	-0.05	0.04		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1388	1dca	A	21	127	3.2e-11	0.27	0.90		RAB GERANYLGERANYLTRANSFERASE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRANSFERASE BETA SUBUNIT; CHAIN: B, D;	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N-FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
1388	1dca	A	46	170	1.6e-12	0.59	0.96		RAB GERANYLGERANYLTRANSFERASE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRANSFERASE BETA SUBUNIT; CHAIN: B, D;	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N-FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
1388	1d59	A	103	236	6.4e-13	0.08	-0.02		OUTER ARM DYNNEIN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE-RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA
1388	1f01	A	41	103	3.2e-06	-0.05	0.40		NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP, RBD OR RRM) AND LEUCINE-RICH-REPEAT 2 (LRR)
1388	1f01	A	89	171	4.8e-07	-0.06	0.10		NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP, RBD OR RRM) AND LEUCINE-RICH-REPEAT 2 (LRR)
1388	1f01	B	41	103	3.2e-06	0.26	0.04		NUCLEAR RNA EXPORT	RNA BINDING PROTEIN TAP (NFX1);

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									FACTOR 1; CHAIN: A, B;	RIBONUCLEOPROTEIN (RNP,RBD OR RRM) AND LEUCINE-RICH-REPEAT 7 (LR8)
1388	1f6v	A	1	173	1.4e-09	0.29	-0.08		SKP2; CHAIN: A, C, E, G, I, K, M, O; SKP1; CHAIN: B, D, F, H, J, L, N, P;	LIGASE CYCLIN A/CDK2-ASSOCIATED PROTEIN P45; CYCLIN A/CDK2-ASSOCIATED PROTEIN P19; SKP1, SKP2, F-BOX, LRR, LEUCINE-RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE
1388	1f6v	A	20	213	1.6e-14	0.12	0.10		SKP2; CHAIN: A, C, E, G, I, K, M, O; SKP1; CHAIN: B, D, F, H, J, L, N, P;	LIGASE CYCLIN A/CDK2-ASSOCIATED PROTEIN P45; CYCLIN A/CDK2-ASSOCIATED PROTEIN P19; SKP1, SKP2, F-BOX, LRR, LEUCINE-RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE
1388	1f6v	A	22	298	4.8e-11	0.08	-0.15		SKP2; CHAIN: A, C, E, G, I, K, M, O; SKP1; CHAIN: B, D, F, H, J, L, N, P;	LIGASE CYCLIN A/CDK2-ASSOCIATED PROTEIN P45; CYCLIN A/CDK2-ASSOCIATED PROTEIN P19; SKP1, SKP2, F-BOX, LRR, LEUCINE-RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE
1388	1f52	A	11	128	3.4e-12	0.21	0.09		SKP2; CHAIN: A, C; SKP1; CHAIN: B, D;	LIGASE CYCLIN A/CDK2-ASSOCIATED P45; CYCLIN A/CDK2-ASSOCIATED P19; SKP1, SKP2, F-BOX, LRRS, LEUCINE-RICH REPEATS, SCF, 2 UBIQUITIN, E3, UBIQUITIN PROTEIN LIGASE
1388	1f52	A	20	213	1.6e-14	0.04	0.03		SKP2; CHAIN: A, C; SKP1; CHAIN: B, D;	LIGASE CYCLIN A/CDK2-ASSOCIATED P45; CYCLIN A/CDK2-ASSOCIATED P19; SKP1, SKP2, F-BOX, LRRS, LEUCINE-RICH REPEATS, SCF, 2 UBIQUITIN, E3, UBIQUITIN PROTEIN LIGASE
1388	2bth		5	131	1.7e-19	0.07	-0.12		RIBONUCLEASE INHIBITOR;	ACETYLATION KINASE INHIBITOR

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									CHAIN: NULL;	RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS
1388	2bnh		74	439	3.2e-20	0.06	-0.15		RIBONUCLEASE INHIBITOR; CHAIN: NULL;	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS
1389	1klo		476	643	1.6e-13	0.05	-0.20		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
1392	1aj4		10	114	3.2e-23	-0.36	0.01		TROPONIN C; CHAIN: NULL;	MUSCLE PROTEIN CTNC: CARDIAC, MUSCLE PROTEIN, REGULATORY, CALCIUM BINDING
1392	1ak8		2	61	3.2e-22	0.21	0.48		CALMODULIN; CHAIN: NULL;	CALCIUM-BINDING PROTEIN CALMODULIN CERUIM TRIC-LOADED, CALCIUM-BINDING PROTEIN
1392	1cdm	A	2	117	4.8e-33	-0.32	0.16		CALCIUM-BINDING PROTEIN CALMODULIN COMPLEXED WITH CALMODULIN-BINDING DOMAIN OF 1CDM 3 CALMODULIN-DEPENDENT PROTEIN KINASE II 1CDM 4 CALCIUM-BINDING PROTEIN CALMODULIN (VERTEBRATE)	
1392	1cll		1	132	3.2e-38			53.74	ICLL 3 CALCIUM-BINDING PROTEIN CALMODULIN (VERTEBRATE)	
1392	1cll		2	117	3.2e-38	-0.37	0.11		CALCIUM-BINDING PROTEIN CALMODULIN (VERTEBRATE) ICLL 3	
1392	1cll	A	10	117	1.6e-21	-0.54	0.12		CARDIAC TROPONIN C; CHAIN: A;	STRUCTURAL PROTEIN HELIX-TURN-HELIX
1392	1exr	A	2	117	1.6e-35	-0.22	0.23		CALMODULIN; CHAIN: A;	METAL TRANSPORT CALMODULIN, HIGH RESOLUTION, DISORDER

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1392	1tef		1	139	3.2e-28			56.30	TROPONIN C; CHAIN: NULL;	CALCIUM-REGULATED MUSCLE CONTRACTION, CALCIUM-BINDING, TROPONIN, E-F HAND, 2 OPEN CONFORMATION, REGULATORY DOMAIN, CALCIUM-REGULATED 3 MUSCLE CONTRACTION
1392	1tef		2	111	3.2e-28	-0.35	0.11		TROPONIN C; CHAIN: NULL;	CALCIUM-REGULATED MUSCLE CONTRACTION, CALCIUM-BINDING, TROPONIN, E-F HAND, 2 OPEN CONFORMATION, REGULATORY DOMAIN, CALCIUM-REGULATED 3 MUSCLE CONTRACTION
1392	1lux		2	111	8e-24	-0.32	0.33		TROPONIN C; ITNX 4 CHAIN: NULL; ITNX 5	CALCIUM-BINDING PROTEIN EF-HAND ITNX 14
1392	1top		1	141	4.8e-28			51.47	CONTRACTILE SYSTEM PROTEIN TROPONIN C ITOP 3	
1392	1top		2	111	4.8e-28	-0.03	0.36		CONTRACTILE SYSTEM PROTEIN TROPONIN C ITOP 3	
1392	1vrk	A	1	135	1.4e-37			51.68	CALMODULIN; CHAIN: A; RS20; CHAIN: B;	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)
1392	1vrk	A	2	117	1.4e-37	-0.42	0.27		CALMODULIN; CHAIN: A; RS20; CHAIN: B;	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)
1396	1b0x	A	934	1000	1.7e-24	1.07	1.00		EP1A4 RECEPTOR TYROSINE KINASE; CHAIN: A;	TRANSFERASE RECEPTOR TYROSINE KINASE, PROTEIN INTERACTION MODULE, 2

SEQ ID NO:	PDB ID	CHAIN N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									CHAIN: B, D;	TRANSDUCTION
1396	1cio		454	531	6e-19	0.32	0.63		GRANULOCYTE COLONY-STIMULATING FACTOR RECEPTOR; CHAIN: NULL; ERYTHROPOIETIN RECEPTOR; CHAIN: A, B;	BINDING PROTEIN BINDING PROTEIN, CYTOKINE RECEPTOR
1396	1em	A	338	531	4.5e-22	-0.12	0.28			CYTOKINE EBP; ERYTHROPOIETIN RECEPTOR, SIGNAL TRANSDUCTION, CYTOKINE 2 RECEPTOR CLASS 1
1396	16of	C	408	531	4.5e-13	-0.05	0.15		PLACENTAL LACTOGEN; CHAIN: A; PROLACTIN RECEPTOR; CHAIN: B, C;	HORMONE/GROWTH FACTOR/HORMONE RECEPTOR 4- HELICAL BUNDLE, ALPHA HELICAL BUNDLE, TERNARY COMPLEX, FN 2 III DOMAINS, BETA SHEET DOMAINS, CYTOKINE-RECEPTOR COMPLEX
1396	1fgk	A	617	900	0			179.56	EGF RECEPTOR 1; CHAIN: A, B;	PHOSPHOTRANSFERASE FGFR1K, FIBROBLAST GROWTH FACTOR RECEPTOR 1; TRANSFERASE, TYROSINE-PROTEIN KINASE, ATP-BINDING, 2 PHOSPHORYLATION, RECEPTOR
1396	1fgk	A	621	895	0	0.91	1.00		FGF RECEPTOR 1; CHAIN: A, B;	PHOSPHOTRANSFERASE FGFRIK, FIBROBLAST GROWTH FACTOR RECEPTOR 1; TRANSFERASE, TYROSINE-PROTEIN KINASE, ATP-BINDING, 2 PHOSPHORYLATION, RECEPTOR
1396	1fgk	B	614	899	0			182.22	FGF RECEPTOR 1; CHAIN: A, B;	PHOSPHOTRANSFERASE FGFRIK, FIBROBLAST GROWTH FACTOR RECEPTOR 1; TRANSFERASE, TYROSINE-PROTEIN KINASE, ATP-BINDING, 2 PHOSPHORYLATION, RECEPTOR

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1396	1fgk	B	620	895	0	0.87	1.00		FGF RECEPTOR 1; CHAIN: A, B;	RECEPTOR, PHOSPHOTRANSFERASE, FIBROBLAST GROWTH FACTOR RECEPTOR 1; TRANSFERASE, TYROSINE-PROTEIN KINASE, ATP-BINDING, 2 PHOSPHORYLATION, RECEPTOR, PHOSPHOTRANSFERASE
1396	1fmk		615	903	0	0.88	1.00		TYROSINE-PROTEIN KINASE SRC; CHAIN: NULL;	PHOSPHOTRANSFERASE C-SRC, P60-SRC; SRC, TYROSINE KINASE, PHOSPHORYLATION, SH2, SH3, 2 PHOSPHOTYROSINE, PROTO-ONCOGENE, PHOSPHOTRANSFERASE
1396	1fna		454	524	1.2e-13	0.39	0.63		CELL ADHESION PROTEIN FIBRONECTIN CELL-ADHESION MODULE TYPE III-10 IFNA 3	PHOSPHOTRANSFERASE
1396	1fnf		322	531	3e-26	0.08	-0.05		FIBRONECTIN; 1FNF 6 CHAIN: NULL; 1FNF 7	CELL ADHESION PROTEIN RGD, EXTRACELLULAR MATRIX 1FNF 18
1396	1fpu	A	623	897	0	0.71	1.00		PROTO-ONCOGENE TYROSINE-PROTEIN KINASE ABL; CHAIN: A, B;	TRANSFERASE P150, C-ABL; KINASE, KINASE INHIBITOR, STI-571, ACTIVATION LOOP
1396	1fr3	A	623	910	0			188.00	INSULIN RECEPTOR; CHAIN: A; PEPTIDE SUBSTRATE; CHAIN: B;	COMPLEX (TRANSFERASE/SUBSTRATE) TYROSINE KINASE, SIGNAL TRANSDUCTION, PHOSPHOTRANSFERASE, 2 COMPLEX (KINASE/PEPTIDE SUBSTRATE/ATP ANALOG), ENZYME, 3 COMPLEX (TRANSFERASE/SUBSTRATE)
1396	1fr3	A	626	910	0	0.81	1.00		INSULIN RECEPTOR; CHAIN: A;	COMPLEX

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									PEPTIDE SUBSTRATE, CHAIN: B;	(TRANSFERASE/SUBSTRATE) TYROSINE KINASE, SIGNAL TRANSDUCTION PHOSPHOTRANSFERASE, 2 COMPLEX (KINASE/PEPTIDE SUBSTRATE/ATP ANALOG), ENZYME, 3 COMPLEX
1396	1inf1		331	533	1.3e-25	0.08	0.53		FIBRONECTIN; CHAIN: NULL;	(TRANSFERASE/SUBSTRATE) CELL ADHESION PROTEIN CELL ADHESION PROTEIN, RGD, EXTRACELLULAR MATRIX, 2 HEPARIN-BINDING, GLYCOPROTEIN
1396	1nuk	A	31	202	1.5e-83	0.58	1.00		TYROSINE-PROTEIN KINASE RECEPTOR EPB; CHAIN: A;	TRANSFERASE NUK; TRANSFERASE, EPB RECEPTOR TYROSINE KINASE,
1396	1nuk	A	31	202	1.5e-83			182.17	TYROSINE-PROTEIN KINASE RECEPTOR EPB; CHAIN: A;	TRANSFERASE NUK; TRANSFERASE, EPB RECEPTOR TYROSINE KINASE,
1396	1qef	A	610	902	0	0.90	1.00		HAEMATOPHOETIC CELL KINASE (ICK); CHAIN: A;	TYROSINE KINASE TYROSINE KINASE-INHIBITOR COMPLEX, DOWN-REGULATED KINASE, 2 ORDERED ACTIVATION LOOP
1396	1qg3	A	329	534	1.5e-36	0.19	0.22		INTEGRIN BETA-4 SUBUNIT; CHAIN: A, B;	STRUCTURAL PROTEIN INTEGRIN, HEMIDESMOSOME, FIBRONECTIN, CARCINOMA, STRUCTURAL 2 PROTEIN
1396	1qg3	A	331	572	6.8e-11	0.03	0.18		INTEGRIN BETA-4 SUBUNIT; CHAIN: A, B;	STRUCTURAL PROTEIN INTEGRIN, HEMIDESMOSOME, FIBRONECTIN, CARCINOMA, STRUCTURAL 2 PROTEIN
1396	1qpe	A	621	900	0	0.97	1.00		LCK KINASE; CHAIN: A;	TRANSFERASE ALPHA BETA FOLD
1396	1qi4	A	331	529	1.5e-30	0.27	-0.03		TENASCIN; CHAIN: A, B;	STRUCTURAL PROTEIN TENASCIN, FIBRONECTIN TYPE-III, HEPARIN,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										EXTRACELLULAR 2 MATRIX, ADHESION, FUSION PROTEIN, STRUCTURAL, PROTEIN
1396	1sgg		934	995	1.7e-25	1.03	1.00		EPHRII, TYPE-B RECEPTOR 2; CHAIN: NULL;	TYROSINE-PROTEIN KINASE NMR, RECEPTOR OLIGOMERIZATION, EPH RECEPTORS, TYROSINE 2 PHOSPHORYLATION, SIGNAL TRANSDUCTION, TYROSINE- PROTEIN 3 KINASE
1396	1ttf		440	524	1e-17	0.13	0.25		GLYCOPROTEIN FIBRONECTIN (TENTH TYPE III MODULE) (NMR, 36 STRUCTURES) ITTF 3	
1396	1vr2	A	622	897	5.1e-98	0.88	1.00		VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR CHAIN: A;	TRANSFERASE KDR; TYROSINE KINASE
1396	2fmb	A	326	423	3e-09	0.07	-0.14		FIBRONECTIN; CHAIN: A;	PROTEIN BINDING ED-B, FIBRONECTIN, TYPEIII DOMAIN, ANGIOGENESIS, PROTEIN 2 BINDING
1396	2fmb	A	439	529	9e-19	0.36	0.17		FIBRONECTIN; CHAIN: A;	PROTEIN BINDING ED-B, FIBRONECTIN, TYPEIII DOMAIN, ANGIOGENESIS, PROTEIN 2 BINDING
1396	2hd		324	524	6e-34	0.22	-0.18		HUMAN TISSUE FACTOR; 2HFT 4 CHAIN: NULL; 2HFT 5	COAGULATION FACTOR
1401	1akb	A	81	121	6e-05	1.11	0.99		MATING-TYPE PROTEIN A-1; CHAINS: A; MATING-TYPE PROTEIN ALPHA-2; CHAIN: B; DNA; CHAIN: C;	COMPLEX (TWO DNA-BINDING PROTEINS/DNA) MAT ALPHA-2; COMPLEX (TWO DNA-BINDING PROTEINS/DNA), COMPLEX, 2 DNA- BINDING PROTEIN, DNA, TRANSCRIPTION REGULATION
1401	1au7	A	83	125	0.00015	0.82	0.94		PTT-1; CHAIN: A; B; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) GHF-1; COMPLEX

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1401	1b72	B	83	125	0.0006	0.27	0.43		HOMEOBOX PROTEIN HOX-B1; CHAIN: A; PBX1; CHAIN: B; DNA CHAIN: D; DNA CHAIN: E; INSULIN GENE ENHANCER PROTEIN ISL-1; CHAIN: NULL; CHAIN: A;	(DNA-BINDING PROTEIN/DNA), PTUTARY, CPED, 2 POU DOMAIN, TRANSCRIPTION FACTOR
1401	1bw5		83	125	6e-05	0.73	0.93			DNA-BINDING PROTEIN ISL-1HD
1401	1da6	A	83	127	0.0003	-0.11	0.03		HOMEOBOX PROTEIN PBX1; CHAIN: A;	DNA-BINDING PROTEIN, HOMEODOMAIN, LIM DOMAIN
1401	1lj	B	83	125	0.0003	0.82	0.99		PAIRED PROTEIN; CHAIN: A, B, C; DNA; CHAIN: D, E, F	COMPLEX (DNA-BINDING PROTEIN/DNA) DNA-BINDING PROTEIN, DNA, PAIRED BOX, TRANSCRIPTION 2 REGULATION
1401	1hdp		83	125	0.00015	0.50	0.80		DNA-BINDING PROTEIN OCT-2 POU HOMEODOMAIN (NMR, AVERAGE STRUCTURE) 1HDP	
1401	1mm	C	82	125	0.00015	0.63	1.00		MCM1 TRANSCRIPTIONAL REGULATOR; CHAIN: A, B; MAT ALPHA-2 TRANSCRIPTIONAL REPRESSOR; CHAIN: C, D; STE6 OPERATOR DNA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION/HOMEOBOX/DNA) PHEROMONE RECEPTOR; MATING-TYPE PROTEIN ALPHA-2; TRANSCRIPTIONAL REGULATION, TRANSCRIPTIONAL REPRESSION, 2 DNA-BINDING PROTEIN, COMPLEX (TRANSCRIPTION/HOMEOBOX/DNA)
1401	1oep		83	125	9e-06	0.28	0.84		OCT-3; IOCP 5 CHAIN: NULL; IOCP 6	DNA-BINDING PROTEIN
1401	1pog		83	125	0.0001	0.41	0.96		DNA BINDING PROTEIN OCT-1 POU HOMEODOMAIN DNA-BINDING PROTEIN MUTANT	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fst Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									WITH IPOG 3 ARG GLY SER HIS MET INSERTED AT THE N-TERMINUS AND ASP ILE IPOG 4 INSERTED AT THE C-TERMINUS (NSRGSIM-ROJINSI(66-DI) IPOG 5 (NMR, 13 STRUCTURES) IPOG 6	
1403	1a36	A	644	772	5.1e-08	0.03	-0.09		TOPOISOMERASE I; CHAIN: A; DNA; CHAIN: B, C;	COMPLEX (ISOMERASE/DNA) COMPLEX (ISOMERASE/DNA), DNA, TOPOISOMERASE I
1403	1dn1	B	389	556	0.00017	-0.16	0.00		SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1A; CHAIN: B;	ENDOCYTOSIS/EXOCYTOSIS NSEC1; PROTEIN-PROTEIN COMPLEX, MULTISUBUNIT
1403	1ec3	A	527	634	0.00017	-0.13	0.19		APOLIPOPROTEIN E; CHAIN: A;	LIPID BINDING PROTEIN APOE3; LIPID TRANSPORT, HEPARIN-BINDING, PLASMA PROTEIN, HDL, VLDL
1403	1quu	A	367	551	6e-15	-0.12	0.04		HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL, CONTRACTILE PROTEIN
1404	1c28	A	826	947	1e-27	1.14	0.39		30 KD ADIPOCYTE COMPLEMENT-RELATED PROTEIN CHAIN: A, B, C;	SERUM PROTEIN ACRP30 C1Q TNF TRIMER ALL-BETA, SERUM PROTEIN
1404	1c28	B	827	947	6e-22	0.71	-0.13		30 KD ADIPOCYTE COMPLEMENT-RELATED PROTEIN CHAIN: A, B, C;	SERUM PROTEIN ACRP30 C1Q TNF TRIMER ALL-BETA, SERUM PROTEIN
1404	1c28	C	826	947	4.5e-18	0.84	0.43		30 KD ADIPOCYTE COMPLEMENT-RELATED PROTEIN CHAIN: A, B, C;	SERUM PROTEIN ACRP30 C1Q TNF TRIMER ALL-BETA, SERUM PROTEIN
1404	1oun	A	375	591	6e-12	-0.03	0.29		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL, LINKER REGION, 2 2

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1404	1cm	A	436	651	4.5e-07	0.02	0.03		ALPHA SPECTRIN; CHAIN: A, B, C;	TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1404	1fo	A	292	467	6e-07	-0.08	0.19		SSO1 PROTEIN; CHAIN: A;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION; 2 2
1404	1hae		120	150	0.0045	0.07	0.11		HEREGULIN-ALPHA; CHAIN: NULL;	TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1404	1hre		120	150	0.0045	0.13	0.25		GROWTH FACTOR HEREGULIN-ALPHA (EPIDERMAL GROWTH FACTOR-LIKE DOMAIN) 1HRE, 3 (NMR, MINIMIZED AVERAGE STRUCTURE) 1HRE 4	MEMBRANE PROTEIN FOUR HELIX BUNDLE, ALPHA HELIX
1407	1b6e	B	25	129	1.4e-09	-0.26	0.12		FK506-BINDING PROTEIN; CHAIN: A, C, E, G; TGF-B SUPERFAMILY RECEPTOR TYPE I; CHAIN: B, D, F, H;	COMPLEX (ISOMERASE/PROTEIN KINASE) FKBP12; SERINE/THREONINE-PROTEIN KINASE RECEPTOR R4; COMPLEX (ISOMERASE/PROTEIN KINASE) RECEPTOR 2 SERINE/THREONINE KINASE
1407	1fgk	A	22	126	1.7e-05	-0.02	0.04		EGF RECEPTOR 1; CHAIN: A, B;	PHOSPHOTRANSFERASE FGFR1K, FIBROBLAST GROWTH FACTOR RECEPTOR 1; TRANSFERASE, TYROSINE-PROTEIN KINASE, ATP-BINDING, 2 PHOSPHORYLATION, RECEPTOR, PHOSPHOTRANSFERASE

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1407	1fmk		22	127	3e-05	0.17	0.36		TYROSINE-PROTEIN KINASE SRC; CHAIN: NULL;	PHOSPHOTRANSFERASE C-SRC, P60-SRC, SRC, TYROSINE KINASE, PHOSPHORYLATION, SH2, SH3, 2, PHOSPHOTYROSINE, PROTO-ONCOGENE, TRANSFERASE
1407	1fpu	A	22	130	1.5e-05	-0.09	0.18		PROTO-ONCOGENE TYROSINE-PROTEIN KINASE ABL; CHAIN: A, B; ERK2; CHAIN: NULL;	PHOSPHOTRANSFERASE P130, C-ABL, KINASE, KINASE INHIBITOR, STI-571, ACTIVATION LOOP
1407	1pme		21	131	7.5e-06	-0.12	0.37			TRANSFERASE MAP KINASE, SERINE/THREONINE PROTEIN KINASE, TRANSFERASE
1407	1qcf	A	22	129	9e-05	-0.56	0.11		HAEMATOPETIC CELL KINASE (HCK); CHAIN: A;	TYROSINE KINASE TYROSINE KINASE-INHIBITOR COMPLEX, DOWN-REGULATED KINASE, 2 ORDERED ACTIVATION LOOP
1407	1qpe	A	22	61	7.5e-05	-0.75	0.23		LCK KINASE; CHAIN: A;	TRANSFERASE ALPHA BETA FOLD
1407	3erk		21	126	1.5e-05	-0.35	0.09		EXTRACELLULAR REGULATED KINASE 2; CHAIN: NULL;	TRANSFERASE MITOGEN ACTIVATED PROTEIN KINASE, MAP 2, ERK2; TRANSFERASE, SERINE/THREONINE-PROTEIN KINASE, MAP KINASE, 2 ERK2
1408	1a44		2	168	4.5e-70	0.60	1.00		PHOSPHATIDYLETHANOLAMINE-BINDING PROTEIN; CHAIN: NULL;	LIPID-BINDING PROTEIN PEBP, PBP LIPID-BINDING
1408	1a44		2	168	4.5e-70			267.15	PHOSPHATIDYLETHANOLAMINE-BINDING PROTEIN; CHAIN: NULL;	LIPID-BINDING PROTEIN PEBP, PBP LIPID-BINDING
1408	1beh	A	3	168	3e-68	0.89	1.00		PHOSPHATIDYLETHANOLAMINE-BINDING PROTEIN; CHAIN: A, B;	LIPID-BINDING LIPID-BINDING, SIGNALLING
1408	1beh	A	3	168	3e-68			271.38	PHOSPHATIDYLETHANOLAMINE-BINDING PROTEIN; CHAIN: NULL;	LIPID-BINDING LIPID-BINDING, SIGNALLING

SEQ NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									A, B;	
1410	1a88	A	47	319	0.00015	0.25	0.90		CHLOROPEPOXIDASE L; CHAIN: A, B, C;	HALOPEPOXIDASE BROMOPEPOXIDASE L; HALOPEPOXIDASE L; HALOPEPOXIDASE; OXIDOREDUCTASE
1410	1a88		47	319	9e-08	0.13	0.45		CHLOROPEPOXIDASE F; CHAIN: NULL;	HALOPEPOXIDASE HALOPEPOXIDASE F; HALOPEPOXIDASE; OXIDOREDUCTASE, PROPIONATE COMPLEX
1410	1azw	A	11	319	4.5e-05			60.20	PROLINE IMINOPEPTIDASE; CHAIN: A, B;	AMINOPEPTIDASE AMINOPEPTIDASE, PROLINE IMINOPEPTIDASE, SERINE PROTEASE, 2 XANTHOMONAS CAMPESTRIS
1410	1azw	A	47	319	4.5e-05	0.00	0.42		PROLINE IMINOPEPTIDASE; CHAIN: A, B;	AMINOPEPTIDASE AMINOPEPTIDASE, PROLINE IMINOPEPTIDASE, SERINE PROTEASE, 2 XANTHOMONAS CAMPESTRIS
1410	1b6g		12	325	1.5e-08			61.14	HALOALKANE DEHALOGENASE; CHAIN: NULL;	HYDROLASE HYDROLASE; HALOALKANE DEHALOGENASE, ALPHA/BETA-HYDROLASE
1410	1b6g		35	318	1.5e-08	0.13	0.77		HALOALKANE DEHALOGENASE; CHAIN: NULL;	HYDROLASE HYDROLASE; HALOALKANE DEHALOGENASE, ALPHA/BETA-HYDROLASE
1410	1eqw	A	10	319	6e-09	0.38	0.99		HALOALKANE DEHALOGENASE; 1- CHLOROHEXANE CHAIN: A;	HYDROLASE AB HYDROLASE FOLD, DEHALOGENASE L5 BOND
1410	1ev2	A	47	154	3e-05	-0.16	0.19		HALOALKANE DEHALOGENASE; CHAIN: A;	HYDROLASE LINB, 1,3,4,6- TETRACHLORO-1,4- CYCLOHEXADIENE

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1410	lek1	A	47	321	1.1e-07	0.12	0.98		EPOXIDE HYDROLASE; CHAIN: A, B;	DEHALOGENASE, LINDANE, BIODEGRADATION, ALPHA/BETA-HYDROLASE
1410	lek1	B	47	321	3e-07	0.14	0.95		EPOXIDE HYDROLASE; CHAIN: A, B;	HYDROLASE HOMODIMER, ALPHA/BETA HYDROLASE FOLD, DISUBSTITUTED UREA 2 INHIBITOR
1410	lilg	A	47	165	0.003	-0.15	0.41		EPOXIDE HYDROLASE; CHAIN: A, B;	HYDROLASE HOMODIMER, ALPHA/BETA HYDROLASE FOLD, DISUBSTITUTED UREA 2 INHIBITOR
1410	lqge	D	47	195	0.0006	-0.13	0.10		LIPASE, GASTRIC; CHAIN: A, B; TRIACYLGLYCEROL	HYDROLASE
									HYDROLASE; CHAIN: D; TRIACYLGLYCEROL	PSEUDOMONADACEAE, CIS-PEPTIDE, CLOSED CONFORMATION, 2 HYDROLASE, LID
1410	lqld	A	47	316	9e-09	0.02	0.37		HYDROXYNITRILE LYASE; CHAIN: A;	LYASE OXYNITRILE LYASE; OXYNITRILASE, CYANOGENESIS, CYANHYDRIN FORMATION, LYASE
1410	lqtr	A	11	321	1.2e-05			57.92	PROLYL AMINOPEPTIDASE; CHAIN: A;	HYDROLASE ALPHA BETA HYDROLASE FOLD, PROLINE, PROLYL AMINOPEPTIDASE, 2 SERRATIA, IMINOPEPTIDASE
1410	lqtr	A	74	319	1.2e-05	-0.51	0.12		PROLYL AMINOPEPTIDASE; CHAIN: A;	HYDROLASE ALPHA BETA HYDROLASE FOLD, PROLINE, PROLYL AMINOPEPTIDASE, 2 SERRATIA, IMINOPEPTIDASE
1410	4lip	D	47	155	9e-05	0.06	0.05		TRIACYLGLYCEROL-HYDROLASE; CHAIN: D, E;	LIPASE LIPASE, LIPASE, HYDROLASE, PSEUDOMONADACEAE, COVALENT INTERMEDIATE, 2 TRIGLYCERIDE ANALOGUE, ENANTIOSELECTIVITY
1415	ldn1	B	384	513	0.00045	-0.02	0.09		SYNTAXIN BINDING PROTEIN I; CHAIN: A; SYNTAXIN 1A;	ENDOCYTOSIS/EXOCYTOSIS NSEC1; PROTEIN-PROTEIN

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									CHAIN: B;	COMPLEX, MULTI-SUBUNIT
1418	1ath	A	401	426	0.00015	0.11	0.01		QGRS ZINC FINGER PEPTIDE; CHAIN: A; DUPLICATION; OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1418	1ath	A	404	485	3e-24	0.05	0.95		QGRS ZINC FINGER PEPTIDE; CHAIN: A; DUPLICATION; OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1418	1mey	C	403	486	4.5e-25			76.20	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1418	1mey	C	404	485	4.5e-25	-0.09	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1418	1mey	C	432	543	6e-23	-0.01	0.53		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1418	1mey	C	461	575	1.2e-21	-0.31	0.06		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1418	1sp1		522	547	1.2e-06	-0.44	0.25		SP1F3; CHAIN: NULL;	ZINC FINGER TRANSCRIPTION FACTOR SP1; ZINC FINGER, TRANSCRIPTION ACTIVATION, SP1 COMPLEX (TRANSCRIPTION)
1418	1ubd	C	408	543	1.4e-24	-0.01	0.07		YY1; CHAIN: C; ADENO-	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fst Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION) REGULATION/DNA)
1418	1ubd	C	432	575	1e-24	-0.42	0.03		YY1; CHAIN: C; ADENOVIRUS ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION) REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION) REGULATION/DNA)
1418	2adr		461	549	4.5e-14	0.04	0.17		ADRI; CHAIN: NULL;	TRANSCRIPTION REGULATION, TRANSCRIPTION REGULATION, ADRI, ZINC FINGER, NMR
1418	2adr		522	575	1.4e-12	-0.41	0.03		ADRI; CHAIN: NULL;	TRANSCRIPTION REGULATION, TRANSCRIPTION REGULATION, ADRI, ZINC FINGER, NMR
1418	2dnp	A	522	577	1.2e-14	-0.69	0.06		COMPLEX (TRANSCRIPTION) REGULATION/DNA) TRAMTRACK PROTEIN (TWO ZINC-FINGER PEPTIDE) COMPLEXED WITH 2DRP 3 DNA 2DRP 4	
1418	2gli	A	369	485	3e-20	-0.05	0.47		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING) PROTEIN/DNA) FIVE-FINGER GLI1; ZINC FINGER, COMPLEX (DNA-BINDING) PROTEIN/DNA)
1418	2gli	A	404	575	4.5e-33	-0.16	0.25		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING) PROTEIN/DNA) FIVE-FINGER GLI1; ZINC FINGER, COMPLEX (DNA-BINDING) PROTEIN/DNA)

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										BINDING PROTEIN/DNA)
1419	1aut	L	118	259	3e-15	0.04	0.17		ACTIVATED PROTEIN C; CHAIN: C, L; D-PHE-PRO-MAI; CHAIN: P;	COMPLEX (BLOOD COAGULATION/INHIBITOR) AUTOPROTHROMBIN IIA; HYDROLASE, SERINE PROTEINASE, PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD COAGULATION/INHIBITOR)
1419	1dan	L	136	270	1.5e-15			57.15	BLOOD COAGULATION FACTOR VIIA; CHAIN: L, H; SOLUBLE TISSUE FACTOR; CHAIN: T, U; D-PHE-PHE-ARG-CHLOROMETHYLKETONE (DFPRCMK) WITH CHAIN: C;	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)
1419	1dx5	I	136	232	1e-17	0.14	0.24		THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN HEAVY CHAIN; CHAIN: M, N; O, P; THROMBOMODULIN; CHAIN: I, J, K, L; THROMBIN INHIBITOR L-GLU-L-GLY-L-ARM; CHAIN: E, F, G, H;	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN, TM, CD141 ANTIGEN; EGR-CMK SERINE PROTEINASE, EGF-LIKE DOMAINS, ANTICOAGULANT COMPLEX, 2 ANTIFIBRINOLYTIC COMPLEX
1419	1dx5	I	168	264	1.1e-13	0.33	0.55		THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN HEAVY CHAIN; CHAIN: M, N; O, P; THROMBOMODULIN; CHAIN: I, J, K, L; THROMBIN INHIBITOR L-GLU-L-GLY-L-ARM; CHAIN: E, F, G, H;	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN, TM, CD141 ANTIGEN; EGR-CMK SERINE PROTEINASE, EGF-LIKE DOMAINS, ANTICOAGULANT COMPLEX, 2 ANTIFIBRINOLYTIC COMPLEX
1419	1ext	A	31	191	3e-16	0.14	-0.11		TUMOR NECROSIS FACTOR RECEPTOR; CHAIN: A, B;	SIGNALLING PROTEIN BINDING PROTEIN, CYTOKINE, SIGNALLING

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1419	1ext	A	61	243	3e-16			59.06	TUMOR NECROSIS FACTOR RECEPTOR; CHAIN: A, B;	PROTEIN
1419	1klo		125	298	9e-22	0.05	-0.01		LAMININ; CHAIN: NULL;	SIGNALLING PROTEIN BINDING
1419	1klo		29	185	4.5e-26	0.34	-0.01		LAMININ; CHAIN: NULL;	PROTEIN, CYTOKINE, SIGNALLING
1419	1klo		61	247	4.5e-27	0.51	0.23		LAMININ; CHAIN: NULL;	PROTEIN
1419	1klo		77	234	4.5e-27			78.19	LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
1419	1pfx	L	13	128	1.1e-25	0.07	-0.09		FACTOR IXA; CHAIN: C, L ₁ ; D-PHE-PRO-ARG; CHAIN: I;	GLYCOPROTEIN GLYCOPROTEIN
										COMPLEX (BLOOD COAGULATION/INHIBITOR)
										CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
1419	1pfx	L	205	298	6e-21	-0.04	0.18		FACTOR IXA; CHAIN: C, L ₁ ; D-PHE-PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR)
										CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
1419	1pfx	L	38	165	6e-30			67.49	FACTOR IXA; CHAIN: C, L ₁ ; D-PHE-PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR)
										CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
1419	1pfx	L	76	223	6e-30	-0.30	0.31		FACTOR IXA; CHAIN: C, L ₁ ; D-PHE-PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR)

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/ECF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
1419	lpp2	R	39	169	1.5e-19	0.24	-0.18		HYDROLASE CALCIUM-FREE PHOSPHOLIPASE A'-2= (EC.3.1.1.4) PP2 4	
1419	lqtk	L	109	216	3e-15	0.11	0.30		COAGULATION FACTOR VILA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VILA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	SERINE PROTEASE FVILA; FVILA; BLOOD COAGULATION, SERINE PROTEASE
1419	lqtk	L	145	247	7.5e-15	0.09	-0.06		COAGULATION FACTOR VILA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VILA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	SERINE PROTEASE FVILA; FVILA; BLOOD COAGULATION, SERINE PROTEASE
1419	lskz		141	271	3e-15	-0.17	0.98		ANTISTASIN; CHAIN: NULL;	SERINE PROTEASE INHIBITOR FACTOR XA INHIBITOR; ANTISTASIN, CRYSTAL STRUCTURE, FACTOR XA INHIBITOR, 2 SERINE PROTEASE INHIBITOR, THROMBOSIS
1419	lskz		66	179	3e-15			55.31	ANTISTASIN; CHAIN: NULL;	SERINE PROTEASE INHIBITOR FACTOR XA INHIBITOR; ANTISTASIN, CRYSTAL STRUCTURE, FACTOR XA INHIBITOR, 2 SERINE PROTEASE INHIBITOR, THROMBOSIS
1419	ltgg		156	237	4.5e-20	0.31	0.53		T-PLASMINOGEN ACTIVATOR	PLASMINOGEN ACTIVATION

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pos Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1419	1tpg		220	297	4.5e-15	-0.31	0.18		FI-G; ITPG 7 CHAIN: NULL; ITPG 8	PLASMINOGEN ACTIVATION
1419	1tpg		29	109	7.5e-19	0.14	-0.01		T-PLASMINOGEN ACTIVATOR FI-G; ITPG 7 CHAIN: NULL; ITPG 8	PLASMINOGEN ACTIVATION
1419	1vap	A	145	273	9e-16	0.02	-0.19		T-PLASMINOGEN ACTIVATOR FI-G; ITPG 7 CHAIN: NULL; ITPG 8	PLASMINOGEN ACTIVATION
1419	1vap	A	81	236	7.5e-16	0.04	-0.19		PHOSPHOLIPASE A2; CHAIN: A, B;	LIPID DEGRADATION PHOSPHOLIPASE A2, LIPID DEGRADATION, HYDROLASE
1419	1vpi		81	204	3e-19	0.07	-0.18		PHOSPHOLIPASE A2 INHIBITOR; CHAIN: NULL.	LIPID DEGRADATION PHOSPHOLIPASE A2, LIPID DEGRADATION, HYDROLASE
1419	1xta	L	145	222	9e-14	0.17	0.37		BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	NEUROTOXIN PHOSPHOLIPASE A2 INHIBITOR, X-RAY STRUCTURE, RECOGNITION, 2 MOLECULAR EVOLUTION, NEUROTOXIN
1419	9wga	A	13	142	1.5e-24	0.23	0.30		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN
1421	1amo	A	272	539	6.8e-40	-0.16	0.01		NADPH-CYTOCHROME P450 REDUCTASE; CHAIN: A, B;	OXIDOREDUCTASE CPR, P450R; X-RAY CRYSTALLOGRAPHY, FLAVOPROTEIN, NITRIC OXIDE SYNTHASE, 2 OXIDOREDUCTASE
1421	1f63	A	252	538	5.1e-57	-0.13	0.21		CHLOROPLAST FERREDOXIN-NADP+ OXIDOREDUCTASE; CHAIN: A, B;	OXIDOREDUCTASE TWO DOMAIN MOTIF; ROSSMANN FOLD

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	FMF score	SEQFOL D score	Compound	PDB annotation
1421	1f5b		252	538	3.4e-55	0.09	0.01		OXIDOREDUCTASE (NADP+ A), FERREDXIN(A)) FERREDXIN:NADP+ OXIDOREDUCTASE (FERREDXIN REDUCTASE, IFNB 3 FLAVOENZYME) (E.C.1.1.1.2) IFNB 4 IFNB 72 FLAVIN REDUCTASE; CHAIN: A, B, C, D;	OXIDOREDUCTASE RIBOFLAVIN, FLAVIN REDUCTASE, FERREDXIN REDUCTASE 2 SUPERFAMILY, OXIDOREDUCTASE
1421	1qfj	A	246	510	3.4e-31	-0.07	0.07		FERREDXIN:NADP+ REDUCTASE; CHAIN: A, B;	OXIDOREDUCTASE FNR; FLAVOENZYME PHOTOSYNTHESIS, ELECTRON TRANSFER, HYDROLYSE 2 TRANSFER, OXIDOREDUCTASE
1421	1qfz	A	252	537	1.7e-54	-0.14	0.43		FERREDXIN:NADP+ REDUCTASE; CHAIN: NULL;	OXIDOREDUCTASE FNR; OXIDOREDUCTASE, FLAVOPROTEIN, NADP, FAD, THYLAKOID MEMBRANE, 2 HYCOBILISOME, FNR, NADP+ REDUCTASE
1421	1que		258	538	3.4e-49	0.06	-0.03		OXIDOREDUCTASE	OXIDOREDUCTASE FNR; OXIDOREDUCTASE, FLAVOPROTEIN, NADP, FAD, THYLAKOID MEMBRANE, 2 HYCOBILISOME, FNR, NADP+ REDUCTASE
1421	2end		244	502	3.4e-57	0.00	-0.12		OXIDOREDUCTASE NITROGENOUS ACCEPTOR NADH-DEPENDENT NITRATE REDUCTASE (CYTOCHROME B REDUCTASE 2CND 3 FRAGMENT) (E.C.1.6.6.1) COMPLEXED WITH FAD 2CND 4 (SYNCHROTRON X-RAY DIFFRACTION) 2CND 5	OXIDOREDUCTASE FNR; OXIDOREDUCTASE, FLAVOPROTEIN, NADP, FAD, THYLAKOID MEMBRANE, 2 HYCOBILISOME, FNR, NADP+ REDUCTASE
1426	1alh	A	265	347	1.5e-45			80.07	QSSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA)

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1426	1mey	C	236	318	1e-51			103.77	OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C; DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	ZINC FINGER, DNA-BINDING PROTEIN COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION; PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1426	1ti5	A	236	402	1.7e-38			99.56	TFIIIA; CHAIN: A, D, 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1426	1ubd	C	211	318	6e-54			88.81	YY1; CHAIN: C; ADENOVIRUS ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1426	2gil	A	207	347	6e-69			93.51	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI, GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1434	1lgl	A	191	320	0.00034	0.41	0.27		STAT3B; CHAIN: A; 18-MER DESOXYOLIGONUCLEOTIDE; CHAIN: B;	COMPLEX (TRANSCRIPTION FACTOR/DNA) TRANSCRIPTION FACTOR, PROTEIN-DNA COMPLEX, CYTOKINE 2 ACTIVATION, COMPLEX (TRANSCRIPTION FACTOR/DNA)
1434	1bz4	A	187	304	1.7e-05	0.25	0.13		APOLIPOPROTEIN E; CHAIN: A;	LIPID BINDING PROTEIN APO-E3;

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										LIPID TRANSPORT, LIPID TRANSPORT, HEPARIN-BINDING, PLASMA 2 PROTEIN, HDL, VLDL REMARK
1434	1c0i		1	514	1.5e-27			115.08	COLICIN 1A; CHAIN: NULL;	TRANSMEMBRANE PROTEIN COLICIN, BACTERIOCIN, ION CHANNEL FORMATION, TRANSMEMBRANE 2 PROTEIN
1434	1cun	A	127	372	7.5e-11	0.07	-0.01		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1434	1cun	A	228	430	3e-10	0.28	0.00		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1434	1cun	A	253	475	3e-11	0.10	0.10		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1434	1cun	A	389	494	6e-06	0.40	0.40		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1434	1dnl	B	296	481	6e-11	0.05	0.18		SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1A; CHAIN: B;	ENDOCYTOSIS/EXOCYTOSIS NSEC1; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT
1434	1ez3	A	316	449	1.5e-08	0.18	-0.18		SYNTAXIN-1A; CHAIN: A, B, C;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELIX

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1434	1ez3	A	364	486	1.5e-08	0.36	-0.02		SYNTAXIN-1A; CHAIN: A, B, C;	BUNDLE ENDOCYTOSIS/EXOCYTOSIS SYNAPOTAGMIN ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELIX BUNDLE TRANSFERASE ALPHA- SUPERHELIX, TRANSFERASE
1434	1qsa	A	2	514	3e-20			104.88	SOLUBLE LYTIC TRANSGLYCOSYLASE SLT70; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE- HELIX COILED COIL, CONTRACTILE PROTEIN TRIPLE- HELIX COILED COIL, CONTRACTILE PROTEIN TRIPLE- HELIX COILED COIL, CONTRACTILE PROTEIN
1434	1quu	A	228	464	1.5e-18	0.21	0.27		HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE- HELIX COILED COIL, CONTRACTILE PROTEIN TRIPLE- HELIX COILED COIL, CONTRACTILE PROTEIN
1434	1quu	A	332	481	1.2e-09	0.25	-0.17		HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE- HELIX COILED COIL, CONTRACTILE PROTEIN
1434	1sig		225	512	3e-09			89.88	RNA POLYMERASE PRIMARY SIGMA FACTOR; CHAIN: NULL;	TRANSCRIPTION REGULATION SIGMA70; RNA POLYMERASE SIGMA FACTOR; TRANSCRIPTION REGULATION
1434	1sig		293	514	3e-09	0.14	0.21		RNA POLYMERASE PRIMARY SIGMA FACTOR; CHAIN: NULL;	TRANSCRIPTION REGULATION SIGMA70; RNA POLYMERASE SIGMA FACTOR, TRANSCRIPTION REGULATION
1437	1rgp		1126	1315	1.5e-53			105.03	RHO GAP; CHAIN: NULL;	G-PROTEIN CDC42 GTPASE- ACTIVATING PROTEIN; G-PROTEIN, GAP, SIGNAL-TRANSDUCTION
1437	1rx4	A	1129	1329	4.5e-58			106.55	P50-RHO GAP; CHAIN: A; TRANSFORMING PROTEIN RHOA; CHAIN: B;	COMPLEX(GTPASE ACTIVATING/PROTO-ONCOGENE) GTPASE-ACTIVATING PROTEIN RHO GAP: COMPLEX (GTPASE ACTIVATING/PROTO-ONCOGENE), GTPASE, 2 TRANSITION STATE, GAP
1441	1ann		7	299	0			431.20	ANNEXIN IV; 1 ANN 5 CHAIN;	CALCIUM/PHOSPHOLIPID-BINDING

SQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast score	Verify score	PMF score	SQFO LD score	Compound	PDB annotation
1447	1dir		9	213	6.8e-55			304.31	OXIDOREDUCTASE(ACTING ON NADH OR NADPH) DIIHYDROPTERINE REDUCTASE (DHPR) (E.C.1.6.99.10) COMPLEX IDHR 3 WITH NADH IDHR 4	PROTEIN 32.5 KDa CALECTRIN, ENDONEXIN I; IANN 7 32.5KD CALECTRIN, ENDONEXIN I, LIPOCORTIN IV, IANN 12 2 CHROMOBINDIN IV, PROTEIN II IANN 13
1452	1b7f	A	1	151	3.4e-33	0.38	0.54		SLXLETHAL PROTEIN; CHAIN: A, B; RNA (5'- R(G)*G(P)*U(p)*G(p)*U(p)*U(p)*U(p)*U(p)*U)-; CHAIN: P, Q;	RNA-BINDING PROTEIN/RNA TRA PRE-MRNA; SPLICING REGULATION, RNP DOMAIN, RNA COMPLEX
1452	1b7f	A	73	230	6.8e-21	0.38	0.99		SLXLETHAL PROTEIN; CHAIN: A, B; RNA (5'- R(G)*G(p)*U(p)*G(p)*U(p)*U(p)*U(p)*U(p)*U)-; CHAIN: P, Q;	RNA-BINDING PROTEIN/RNA TRA PRE-MRNA; SPLICING REGULATION, RNP DOMAIN, RNA COMPLEX
1452	1b7f	A	73	252	6.8e-21			51.11	SLXLETHAL PROTEIN; CHAIN: A, B; RNA (5'- R(p)*G(p)*U(p)*G(p)*U(p)*U(p)*U(p)*U(p)*U)-; CHAIN: P, Q;	RNA-BINDING PROTEIN/RNA TRA PRE-MRNA; SPLICING REGULATION, RNP DOMAIN, RNA COMPLEX
1452	1evj	A	1	156	3.4e-46			52.06	POLYDENYLATE BINDING PROTEIN I; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(C)*A(p)*A(p)*A(p)*A(p)*A(p)*A(p)*A(p)*A(p)*A)-; CHAIN: M, N, O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN I; PARP I; REM; PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
1452	1evj	A	5	157	3.4e-46	0.27	0.80		POLYDENYLATE BINDING PROTEIN I; CHAIN: A, B, C, D,	GENE REGULATION/RNA POLY(A) BINDING PROTEIN I; PARP I; REM

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SQFOLO D score	Coumpound	PDB annotation
1452	1evj	H	77	159	1.7e-19	0.81	1.00		POLYDENVYLATE BINDING PROTEIN I; CHAIN: A, B, C, D, E, F, G, H; RNA (5'-R(C [*] AP [*] AP [*] A [*] P [*] AP [*] A [*] P [*] AP [*] A [*] P [*] A [*])-3'); CHAIN: M, N, O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN I, PAPB I; REM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
1452	1d8z	A	73	153	1.7e-21	0.73	1.00		HU ANTIGEN C; CHAIN: A;	RNA BINDING PROTEIN RNA-BINDING DOMAIN
1452	1ha1	-	1	151	1.7e-35	0.06	0.07		HNRNP A1; CHAIN: NULL;	NUCLEAR PROTEIN HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1, NUCLEAR PROTEIN, HNRNP, RBD, RRM, RNP, RNA BINDING, 2 RIBONUCLEOPROTEIN
1452	1ha1	-	75	157	1.7e-21	0.87	1.00		HNRNP A1; CHAIN: NULL;	NUCLEAR PROTEIN HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1, NUCLEAR PROTEIN, HNRNP, RBD, RRM, RNP, RNA BINDING, 2 RIBONUCLEOPROTEIN
1452	2o2f	A	74	158	3.4e-19			30.59	SPLICING FACTOR UZAF 65 KD SUBUNIT; CHAIN: A;	RNA-BINDING PROTEIN SPLICING, U2 SNRNP, RBD, RNA-BINDING PROTEIN
1452	2up1	A	1	155	1.2e-36	0.28	0.64		HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1; CHAIN: A; 12-NUCLEOTIDE SINGLE-STRANDED TELEOMETRIC DNA; CHAIN: B;	COMPLEX (RIBONUCLEOPROTEIN/DNA) HNRNP A1, UP1; COMPLEX (RIBONUCLEOPROTEIN/DNA), HETEROGENEOUS NUCLEAR 2 RIBONUCLEOPROTEIN A1
1452	3axl	A	1	144	3.4e-32	0.13	0.04		SEX-LETHAL; CHAIN: A, B, C;	RNA BINDING DOMAIN RNA BINDING DOMAIN, RBD, RNA RECOGNITION MOTIF, RRM, 2 SPLICING INHIBITOR, TRANSLATIONAL INHIBITOR, SEX-3

SEQ NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1452	3sl	A	76	230	1.4e-20	0.20	0.69		SEX-LETHAL; CHAIN: A, B, C;	DETERMINATION, X CHROMOSOME DOSAGE COMPENSATION RNA BINDING DOMAIN RNA BINDING DOMAIN, RBD, RNA RECOGNITION MOTIF, RRM, 2 SPLICING INHIBITOR, TRANSLATIONAL INHIBITOR, SEX 3 DETERMINATION, X CHROMOSOME DOSAGE COMPENSATION
1452	3sl	A	7	146	3.4e-32			53.30	SEX-LETHAL; CHAIN: A, B, C;	RNA BINDING DOMAIN RNA BINDING DOMAIN, RBD, RNA RECOGNITION MOTIF, RRM, 2 SPLICING INHIBITOR, TRANSLATIONAL INHIBITOR, SEX 3 DETERMINATION, X CHROMOSOME DOSAGE COMPENSATION
1454	1c0k	A	345	668	3.4e-85	-0.04	0.87		HIV-1 REVERSE TRANSCRIPTASE (A-CHAIN); CHAIN: A; HIV-1 REVERSE TRANSCRIPTASE (B-CHAIN); CHAIN: B;	TRANSFERASE HIV-1 REVERSE TRANSCRIPTASE, AIDS, NON-NUCLEOSIDE INHIBITOR, 2 DRUG DESIGN
1454	1c0k	B	346	668	5.1e-88	-0.17	0.84		HIV-1 REVERSE TRANSCRIPTASE (A-CHAIN); CHAIN: A; HIV-1 REVERSE TRANSCRIPTASE (B-CHAIN); CHAIN: B;	TRANSFERASE HIV-1 REVERSE TRANSCRIPTASE, AIDS, NON-NUCLEOSIDE INHIBITOR, 2 DRUG DESIGN
1454	1c1e	B	345	668	0	-0.09	0.99		HIV-1 REVERSE TRANSCRIPTASE (A-CHAIN); CHAIN: A; HIV-1 REVERSE TRANSCRIPTASE (B-CHAIN); CHAIN: B;	TRANSFERASE HIV-1 REVERSE TRANSCRIPTASE, AIDS, NON-NUCLEOSIDE INHIBITOR, 2 DRUG DESIGN
1454	1c9r	A	341	671	1.7e-91	-0.06	0.99		HIV-1 REVERSE TRANSCRIPTASE (CHAIN A);	TRANSFERASE/IMMUNE SYSTEM/MDNA HIV-1 RT; HIV-1 RT;

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SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									CHAIN: A; HIV-1 REVERSE TRANSCRIPTASE (CHAIN B); CHAIN: B; ANTIBODY (LIGHT CHAIN); CHAIN: L; ANTIBODY (HEAVY CHAIN); CHAIN: H; DNA (5'- CHAIN: T; DNA (5'- CHAIN: P;	HIV, REVERSE TRANSCRIPTASE, MET184ILE, 3TC, PROTEIN-DNA 2 COMPLEX, DRUG RESISTANCE, M184I, TRANSFERASE/IMMUNE 3 SYSTEM/DNA
1454	1c9r	B	341	668	8.5e-98	-0.13	0.99		HIV-1 REVERSE TRANSCRIPTASE (CHAIN A); CHAIN: A; HIV-1 REVERSE TRANSCRIPTASE (CHAIN B); CHAIN: B; ANTIBODY (LIGHT CHAIN); CHAIN: L; ANTIBODY (HEAVY CHAIN); CHAIN: H; DNA (5'- CHAIN: T; DNA (5'- CHAIN: P;	TRANSFERASE/IMMUNE SYSTEM/DNA HIV-1 RT; HIV-1 RT; HIV, REVERSE TRANSCRIPTASE, MET184ILE, 3TC, PROTEIN-DNA 2 COMPLEX, DRUG RESISTANCE, M184I, TRANSFERASE/IMMUNE 3 SYSTEM/DNA
1454	1lar		341	551	3.4e-65	0.05	1.00		REVERSE TRANSCRIPTASE HIV-1 REVERSE TRANSCRIPTASE (AMINO-TERMINAL HALF) (FINGERS IHAR 3 AND PALM SUBDOMAINS) (R1216) (E.C.2.7.7.49) IHAR 4	REVERSE TRANSCRIPTASE
1454	1mm1		326	570	1e-59	0.36	1.00		MMLV REVERSE TRANSCRIPTASE; 1MML 4 CHAIN: NULL; 1MML 5	REVERSE TRANSCRIPTASE
1454	1mm1		326	571	1e-59			199.34	MMLV REVERSE TRANSCRIPTASE; 1MML 4 CHAIN: NULL; 1MML 5	REVERSE TRANSCRIPTASE
1454	1rth	A	341	668	0	0.00	1.00		HIV-1 REVERSE TRANSCRIPTASE; IRTH 4 CHAIN: A; B; IRTH 5	NUCLEOTIDYLTRANSFERASE HIV-1 RT; IRTH 6 HIV-1 REVERSE TRANSCRIPTASE IRTH 15
1454	1rth	B	345	668	0	-0.17	1.00		HIV-1 REVERSE TRANSCRIPTASE; IRTH 4	NUCLEOTIDYLTRANSFERASE HIV-1 RT; IRTH 6 HIV-1 REVERSE

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Bias	Verify score	FMF score	SEQFOL D score	Compound	PDB annotation
1454	1vrt	A	345	568	0	-0.04	1.00		CHAIN: A, B, 1RTH 5 HIV-1 REVERSE TRANSCRIPTASE; 1VRT 4 CHAIN: A, B, 1VRT 3	TRANSCRIPTASE 1RTH 15 NUCLEOTIDYLTRANSFERASE HIV-1 RT; 1VRT 6 HIV-1 REVERSE TRANSCRIPTASE 1VRT 15
1454	1vrt	B	345	568	0	-0.09	1.00		HIV-1 REVERSE TRANSCRIPTASE; 1VRT 4 CHAIN: A, B, 1VRT 5	NUCLEOTIDYLTRANSFERASE HIV-1 RT; 1VRT 6 HIV-1 REVERSE TRANSCRIPTASE 1VRT 15
1454	3hvt	B	342	568	3.4e-100	-0.11	0.66		NUCLEOTIDYLTRANSFERASE REVERSE TRANSCRIPTASE (E.C.2.7.7.49) 3HVT 3	
1454	3hvt	B	342	572	3.4e-100			84.10	NUCLEOTIDYLTRANSFERASE REVERSE TRANSCRIPTASE (E.C.2.7.7.49) 3HVT 3	
1455	1dus	A	6	135	5.1e-13	-0.00	-0.08		MJ0882; CHAIN: A;	STRUCTURAL GENOMICS HYPOTHETICAL PROTEIN; METHANOCOCCUS JANNASCHII
1456	1igl		25	94	6.8e-25	0.37	1.00		GROWTH FACTOR INSULIN-LIKE GROWTH FACTOR II (IGF-II, IGF-2) 1IGL 3 (NMR, 20 STRUCTURES) 1IGL 4 1IGL 78	
1456	1igl		25	94	6.8e-25			108.25	GROWTH FACTOR INSULIN-LIKE GROWTH FACTOR II (IGF-II, IGF-2) 1IGL 3 (NMR, 20 STRUCTURES) 1IGL 4 1IGL 78	
1456	3iri	A	16	93	4.5e-25	-0.15	1.00		INSULIN-LIKE GROWTH FACTOR 1; CHAIN: A;	GROWTH FACTOR INSULIN-LIKE GROWTH FACTOR-1, GROWTH FACTOR, NMR, PROTEIN 2 STRUCTURE, DISTANCE GEOMETRY
1458	2oc	E	46	132	6.8e-37	0.33	1.00		CYTOCHROME C OXIDASE; CHAIN: A, B, C, D, E, F, G, H, I, J	OXIDOREDUCTASE FERROCYTOCHROME C/OXYGEN

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									K, L, M, N, O, P, Q,	OXIDOREDUCTASE; OXIDOREDUCTASE; CYTOCHROME C OXYGEN, CYTOCHROME C 2 OXIDASE
1458	2occ	E	46	132	6.8e-37			115.24	CYTOCHROME C OXIDASE; CHAIN: A, B, C, D, E, F, G, H, I, J, K, L, M, N, O, P, Q,	OXIDOREDUCTASE FERROCYTOCHROME C OXYGEN OXIDOREDUCTASE; OXIDOREDUCTASE; CYTOCHROME C OXYGEN, CYTOCHROME C 2 OXIDASE
1459	1avs	A	601	640	0.009	0.64	1.00		TROPONIN C; CHAIN: A, B;	MUSCLE CONTRACTION MUSCLE CONTRACTION, CALCIUM- ACTIVATED, TROPONIN, E-F HAND 2 CALCIUM-BINDING PROTEIN
1459	1avj		332	408	3e-11	0.01	0.29		ITK; CHAIN: NULL;	TRANSFERASE II-2-INDUCIBLE T- CELL KINASE; TRANSFERASE, REGULATORY INTRAMOLECULAR COMPLEX, KINASE
1459	1b8q	A	248	365	1e-18	-0.14	0.87		NEURONAL NITRIC OXIDE SYNTHASE; CHAIN: A; HEPTAPEPTIDE; CHAIN: B;	OXIDOREDUCTASE PDZ DOMAIN, NOS, NITRIC OXIDE SYNTHASE
1459	1be9	A	248	341	3.4e-16	0.28	0.92		PSD-95; CHAIN: A; CRPT; CHAIN: B;	PEPTIDE RECOGNITION PEPTIDE RECOGNITION, PROTEIN LOCALIZATION
1459	1g2b	A	334	392	3e-12	-0.25	0.54		SPECTRIN ALPHA CHAIN; CHAIN: A;	METAL BINDING PROTEIN CAPPING PROTEIN, CALCIUM-BINDING, DUPLICATION, REPEAT, SH 2 DOMAIN, CYTOSKELETON
1459	1gdr	A	340	408	4.5e-11	-0.16	0.13		SIGNAL TRANSDUCTION PROTEIN GROWTH FACTOR RECEPTOR-BOUND PROTEIN 2 (GRB2, N-TERMINAL, IGBR 3 SH3 DOMAIN) COMPLEXED	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									WITH SOS-A PEPTIDE 1GBR 4 (NMR, 29 STRUCTURES) 1GBR 5	
1459	1gfc		349	408	1e-10	0.36	0.66		ADAPTOR PROTEIN CONTAINING SH2 AND SH3 GROWTH FACTOR RECEPTOR-BOUND PROTEIN 2 (GRB2) :GFC 3 (C-TERMINAL SH3 DOMAIN) (NMR, MINIMIZED MEAN STRUCTURE) 1GFC 4	
1459	1gky		479	663	1e-68			146.00	TRANSFERASE GUANYLATE KINASE (E.C.2.7.4.8) COMPLEX WITH 1GKY 3 GUANOSINE MONOPHOSPHATE 1GKY 4	
1459	1gky		480	662	1e-68	0.80	1.00		TRANSFERASE GUANYLATE KINASE (E.C.2.7.4.8) COMPLEX WITH 1GKY 3 GUANOSINE MONOPHOSPHATE 1GKY 4	
1459	1i16		253	345	1.1e-16	0.31	0.95		INTERLEUKIN 16; CHAIN: NULL;	CYTOKINE LCF; CYTOKINE, LYMPHOCYTE CHEMOATTRACTANT FACTOR, PDZ DOMAIN
1459	1kwa	A	254	337	3e-17	0.19	1.00		HCASK/LIN-2 PROTEIN; CHAIN: A, B;	KINASE HCASK, GLGF REPEAT; DHR; PDZ DOMAIN; NEUREXIN, SYNDRECAN, RECEPTOR CLUSTERING, KINASE
1459	1kwa	A	257	338	3.4e-16	0.07	0.98		HCASK/LIN-2 PROTEIN; CHAIN: A, B;	KINASE HCASK, GLGF REPEAT; DHR; PDZ DOMAIN; NEUREXIN, SYNDRECAN, RECEPTOR CLUSTERING, KINASE
1459	1pdr		253	342	3.4e-14	0.19	0.96		HUMAN DISCS LARGE PROTEIN; CHAIN: NULL;	SIGNAL TRANSDUCTION HDLG, DHR3 DOMAIN; SIGNAL TRANSDUCTION, SH3 DOMAIN, REPEAT

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	FMF score	SEQFOL D score	Compound	PDB annotation
1459	lpwt		347	408	4.5e-11	0.46	0.58		ALPHA SPECTRIN; CHAIN: NULL;	CIRCULAR PERMUTANT PWT; CIRCULAR PERMUTANT, SH3 DOMAIN, CYTOSKELETON
1459	lqau	A	254	362	1.5e-17	0.13	0.98		NEURONAL NITRIC OXIDE SYNTHASE (RESIDUES 1-130); CHAIN: A;	OXIDOREDUCTASE BETA-FINGER
1459	lqv	A	250	336	4.5e-16	0.24	1.00		ALPHA-1 SYNTROPHIN (RESIDUES 77-171); CHAIN: A; NEURONAL NITRIC OXIDE SYNTHASE (RESIDUES 1-130); CHAIN: B;	MEMBRANE PROTEIN/OXIDOREDUCTASE BETA-FINGER, HETERODIMER
1459	lqlw	A	350	408	3e-11	0.10	0.48		ALPHA II SPECTRIN; CHAIN: A;	CYTOSKELETON CYTOSKELETON, MEMBRANE, SH3 DOMAIN
1459	lqlv	A	349	408	1.3e-10	0.41	0.47		TYROSINE-PROTEIN KINASE BTK; CHAIN: A;	TYROSINE-PROTEIN KINASE BRUTON'S TYROSINE KINASE, B CELL PROGENITOR KINASE, TRANSFERASE, TYROSINE-PROTEIN KINASE, PHOSPHORYLATION, 2 SH3 DOMAIN
1459	lsem	A	350	408	1.5e-10	-0.10	0.41		SEM-5; ISEM 3 CHAIN: A, B; ISEM 5 10-RESIDUE PROLINE-RICH PEPTIDE FROM MSOS ISEM 8 CHAIN: C, D ISEM 10	SIGNAL TRANSDUCTION PROTEIN SRC-HOMOLOGY 3 (SH3) DOMAIN, PEPTIDE-BINDING PROTEIN, ISEM 18 2 GUANINE NUCLEOTIDE EXCHANGE FACTOR ISEM 19
1459	lind		334	392	6e-13	0.22	0.40		ALPHA-SPECTRIN; CHAIN: NULL;	CYTOSKELETON CAPPING PROTEIN, CALCIUM-BINDING, DUPLICATION REPEAT, 2 SH3 DOMAIN, CYTOSKELETON
1459	lukz		477	659	1.4e-07	0.10	0.69		TRANSFERASE URIDYLATE KINASE (E.C.2.7.4.-) COMPLEXED WITH ADP AND AMP IUKZ 3.	
1459	lzan	A	482	662	1.2e-05	0.02	0.22		ADENYLATE KINASE; CHAIN:	TRANSFERASE ATP-AMP-

SEQ NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1459	3adk		475	662	9e-06	0.12	0.98		A, B;	PHOSPHOTRANSFERASE, TRANSFERASE
1459	3pdz	A	253	332	1.5e-13	0.32	1.00		TRANSFERASE(PHOSPHOTRANSFERASE) ADENYLATE KINASE (B.C.2.7.4.3) 3ADK 4	HYDROLASE PDZ DOMAIN, HUMAN PHOSPHATASE, HPPT1E, PTP-BAS, SPECIFICITY 2 OF BINDING
1459	3mk	C	479	662	9e-10	0.28	0.04		TYROSINE PHOSPHATASE (PTP-BAS, TYPE 1); CHAIN: A;	KINASE KINASE, PHOSPHOTRANSFERASE
1459	4mk	A	478	662	7.5e-16	-0.03	0.19		THYMIDYLATE KINASE; CHAIN: A, B, C, D, E, F, G, H;	TRANSFERASE ATP:DTMP
									THYMIDYLATE KINASE; CHAIN: A;	PHOSPHOTRANSFERASE
1461	1bg3	A	1	498	0	1.13	1.00		HEXOKINASE; CHAIN: A, B;	HEXOKINASE ATP/D-HEXOSE-6-PHOSPHOTRANSFERASE, HEXOKINASE, PHOSPHOTRANSFERASE
1461	1bg3	A	1	499	0			459.01	HEXOKINASE; CHAIN: A, B;	HEXOKINASE ATP/D-HEXOSE-6-PHOSPHOTRANSFERASE; HEXOKINASE, PHOSPHOTRANSFERASE
1461	1cza	N	1	501	0	1.07	1.00		HEXOKINASE TYPE I; CHAIN: N;	TRANSFERASE STRUCTURALLY HOMOLOGOUS DOMAINS
1464	1a0j	A	30	239	1.4e-80	0.88	1.00		TRYPSIN; CHAIN: A, B, C, D;	SERINE PROTEINASE SERINE PROTEINASE, TRYPSIN, HYDROLASE
1464	1a0j	A	30	239	1.4e-80			104.84	TRYPSIN; CHAIN: A, B, C, D;	SERINE PROTEINASE SERINE PROTEINASE, TRYPSIN, HYDROLASE
1464	1a0l	A	30	233	1.7e-74	0.50	1.00		BETA-TRYPTASE; CHAIN: A, B, C, D;	SERINE PROTEINASE TRYPSIN-LIKE SERINE PROTEINASE, TETRAMER, HEPARIN, ALLERGY, 2 ASTHMA
1464	1a0l	A	30	239	1.7e-74			97.00	BETA-TRYPTASE; CHAIN: A, B;	SERINE PROTEINASE TRYPSIN-LIKE

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1464	1bru	P	30	239	1.7e-75	0.64	1.00		C, D;	SERINE PROTEINASE, TETRAMER, HEPARIN ALLERGY, 2 ASTHMA
1464	1bru	P	30	239	1.7e-75			115.93	ELASTASE; CHAIN: P;	SERINE PROTEASE PPE; SERINE PROTEASE, HYDROLASE
1464	1dpo		30	239	1.7e-79			98.94	ELASTASE; CHAIN: P;	SERINE PROTEASE PPE; SERINE PROTEASE, HYDROLASE
									TRYPSIN; CHAIN: NULL;	SERINE PROTEASE HYDROLASE, SERINE PROTEASE, DIGESTION, PANCREAS, ZYMOGEN, 2 SIGNAL, MULTIGENE FAMILY
1464	1fuj	A	30	237	6e-71			200.42	PR3; CHAIN: A, B, C, D;	HYDROLASE (SERINE PROTEASE) MYELOBLASTIN; HYDROLASE, SERINE PROTEASE, GLYCOPROTEIN, ZYMOGEN, SIGNAL
1464	1mct	A	30	239	8.5e-83	0.74	1.00		COMPLEX(TRYPSINASE/INHIBITOR) TRYPSIN (E.C.3.4.21.4) COMPLEXED WITH INHIBITOR FROM BITTER IMCT 3 GOURD IMCT 4	
1464	1mct	A	30	239	8.5e-83			103.86	COMPLEX(TRYPSINASE/INHIBITOR) TRYPSIN (E.C.3.4.21.4) COMPLEXED WITH INHIBITOR FROM BITTER IMCT 3 GOURD IMCT 4	
1464	1ppf	E	30	237	1e-65			315.52	HYDROLASE(SERINE PROTEINASE) HUMAN LEUKOCYTE ELASTASE (HLE) NEUTROPHIL ELASTASE (HNE) IPPF 3 (E.C.3.4.21.37) COMPLEX WITH THE THIRD DOMAIN OF TURKEY IPPF 4 OVOMUCOID INHIBITOR (OMTKY3) IPPF 5	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1464	1qz	A	12	239	3.4e-71			117.30	PLASMINOGEN; CHAIN: A, B, C, D;	HYDROLASE MICROPLASMINOGEN, SERINE PROTEASE, ZYMOMEN, CHYMOTRYPSIN 2 FAMILY, HYDROLASE
1464	1sgf	G	30	239	3.4e-72	0.65	1.00		NERVE GROWTH FACTOR; CHAIN: A, B, G, X, Y, Z;	GROWTH FACTOR 7S NGF; GROWTH FACTOR (BETA-NGF), HYDROLASE - SERINE PROTEINASE 2 (GAMMA-NGF), INACTIVE SERINE PROTEINASE (ALPHA-NGF)
1464	1sgf	G	30	240	3.4e-72			97.78	NERVE GROWTH FACTOR; CHAIN: A, B, G, X, Y, Z;	GROWTH FACTOR 7S NGF; GROWTH FACTOR (BETA-NGF), HYDROLASE - SERINE PROTEINASE 2 (GAMMA-NGF), INACTIVE SERINE PROTEINASE (ALPHA-NGF)
1464	1slw	B	30	239	1.7e-78	0.45	1.00		ECOTIN; CHAIN: A; ANIONIC TRYPSIN; CHAIN: B;	COMPLEX SERINE PROTEASE/INHIBITOR TRYPSIN INHIBITOR; SERINE PROTEASE, INHIBITOR, COMPLEX, METAL BINDING SITES, 2 PROTEIN ENGINEERING, PROTEASE- SUBSTRATE INTERACTIONS, 3 METALLOPROTEINS
1464	1tm	A	30	239	5.1e-80	0.79	1.00		HYDROLASE (SERINE PROTEINASE) TRYPSIN (E.C.3.4.21.4) COMPLEXED WITH THE INHIBITOR ITRN 3 DIISOPROPYL- FLUOROPHOSPHORFLUORIDAT E (DPP) ITRN 4 HUMAN TRYPSIN, DPP INHIBITED ITRN 6	
1464	1tm	A	30	240	5.1e-80			100.94	HYDROLASE (SERINE PROTEINASE) TRYPSIN	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									(E.C.3.4.21.4) COMPLEXED WITH THE INHIBITOR ITRN 3 DIISOPROPYL- FLUOROPHOSPHORODAT E (DFP) ITRN 4 HUMAN TRYPSIN, DFP INHIBITED ITRN 6	
1464	2lts		30	237	5.1e-79	0.65	1.00		HYDROLASE(SERINE PROTEINASE) TRYPSIN (E.C.3.4.21.4) COMPLEXED WITH BENZAMIDINE INHIBITOR 2TBS 3	
1464	2lts		30	239	5.1e-79			97.32	HYDROLASE(SERINE PROTEINASE) TRYPSIN (E.C.3.4.21.4) COMPLEXED WITH BENZAMIDINE INHIBITOR 2TBS 3	
1464	5pp		30	239	1.7e-76	0.73	1.00		BETA TRYPSIN; CHAIN: NULL;	SERINE PROTEASE HYDROLASE, SERINE PROTEASE, DIGESTION, PANCREAS, 2 ZYMOGEN, SIGNAL
1464	5pp		30	239	1.7e-76			99.14	BETA TRYPSIN; CHAIN: NULL;	SERINE PROTEASE HYDROLASE, SERINE PROTEASE, DIGESTION, PANCREAS, 2 ZYMOGEN, SIGNAL
1470	1a4e	A	3	229	1.7e-98			234.97	14-3-3 PROTEIN ZETA; CHAIN: A, B, C, D;	SIGNAL TRANSDUCTION SIGNAL TRANSDUCTION
1470	1a4e	A	3	230	1.7e-98	0.55	1.00		14-3-3 PROTEIN ZETA; CHAIN: A, B, C, D;	SIGNAL TRANSDUCTION SIGNAL TRANSDUCTION
1470	1q1a	A	3	232	0	0.59	1.00		14-3-3 PROTEIN ZETA; CHAIN: A, B; PHOSPHOPEPTIDE; CHAIN: Q, R	COMPLEX (SIGNAL TRANSDUCTION/PEPTIDE) COMPLEX, 14-3-3, PHOSPHOPEPTIDE, SIGNAL TRANSDUCTION
1470	1q1a	A	3	232	0			284.35	14-3-3 PROTEIN ZETA; CHAIN:	COMPLEX (SIGNAL

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									A, B; PHOSPHOPEPTIDE; CHAIN: Q, R	TRANSDUCTION(P/PEPTIDE) COMPLEX, 14-3-3, PHOSPHOPEPTIDE, SIGNAL TRANSDUCTION
1471	1cii		48	621	3.4e-08			133.38	COLICIN 1A; CHAIN: NULL;	TRANSMEMBRANE PROTEIN COLICIN, BACTERIOCIN, ION CHANNEL FORMATION,
1471	1cum	A	117	322	6e-15	-0.15	0.03		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1471	1cum	A	152	363	7.5e-16	0.12	-0.17		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1471	1cum	A	38	248	3e-20	0.05	0.39		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1471	1ez3	A	23	139	1.5e-09	0.19	-0.13		SYNTAXIN-1A; CHAIN: A, B, C;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELIX BUNDLE
1471	1ez3	A	95	214	4.5e-08	0.01	-0.15		SYNTAXIN-1A; CHAIN: A, B, C;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELIX BUNDLE
1471	1lqu	A	196	426	6e-19	0.02	0.11		HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL.

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1471	1lqn	A	217	487	1.5e-15	0.09	-0.02		HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN HELIX COILED COIL CONTRACTILE PROTEIN
1471	1sig		32	307	6e-09	-0.11	0.03		RNA POLYMERASE PRIMARY SIGMA FACTOR; CHAIN: NULL;	TRANSCRIPTION REGULATION SIGMA70: RNA POLYMERASE SIGMA FACTOR, TRANSCRIPTION REGULATION
1475	1nfi	E	23	77	0.0045	-0.56	0.04		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1476	1cm	A	150	337	3e-06	-0.18	0.15		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 22 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1476	1cm	A	241	458	9e-13	-0.12	0.19		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 22 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1476	1cm	A	460	687	1.5e-15	-0.05	0.55		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 22 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1476	1cm	A	506	724	4.5e-15	0.19	0.35		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 22 TANDEM 3-HELIX COILED-COILS,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1476	1cun	A	563	794	9e-17	0.15	0.42		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1476	1cun	A	652	850	1.2e-13	0.08	0.09		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1476	1cun	A	721	916	6e-12	-0.00	-0.14		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1476	1dn1	B	216	423	6e-16	0.03	-0.05		SYNTAXIN BINDING PROTEIN I; CHAIN: A; SYNTAXIN 1A; CHAIN: B;	ENDOCYTOSIS/EXOCYTOSIS NSEC; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT
1476	1dn1	B	380	597	1.5e-16	-0.30	0.01		SYNTAXIN BINDING PROTEIN I; CHAIN: A; SYNTAXIN 1A; CHAIN: B;	ENDOCYTOSIS/EXOCYTOSIS NSEC; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT
1476	1dn1	B	503	711	6e-18	-0.21	0.06		SYNTAXIN BINDING PROTEIN I; CHAIN: A; SYNTAXIN 1A; CHAIN: B;	ENDOCYTOSIS/EXOCYTOSIS NSEC; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT
1476	1dn1	B	700	911	6e-13	-0.19	0.03		SYNTAXIN BINDING PROTEIN I; CHAIN: A; SYNTAXIN 1A; CHAIN: B;	ENDOCYTOSIS/EXOCYTOSIS NSEC; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT
1476	1ez3	A	256	363	3e-07	-0.26	0.03		SYNTAXIN-1A; CHAIN: A, B, C;	ENDOCYTOSIS/EXOCYTOSIS NSEC; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT
1476	1ez3	A	593	719	1.5e-11	0.00	-0.06		SYNTAXIN-1A; CHAIN: A, B, C;	ENDOCYTOSIS/EXOCYTOSIS NSEC; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1476	1ez3	A	704	822	4.5e-10	0.28	0.19		SYNTAXIN-1A; CHAIN: A, B, C;	KDA PROTEIN, P35A, THREE HELIX BUNDLE
1476	1fio	A	491	648	9e-10	0.17	0.15		SSO1 PROTEIN; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAMIN ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELIX BUNDLE
1476	1f6k	C	548	711	0.0001	-0.29	0.59		PREFOLDIN; CHAIN: A; PREFOLDIN; CHAIN: B; PREFOLDIN; CHAIN: C;	MEMBRANE PROTEIN FOUR HELIX BUNDLE, ALPHA HELIX
1476	1quu	A	320	573	4.5e-22	-0.19	0.00		HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CHAPERONE ARCHAEAL PROTEIN
1476	1quu	A	390	640	3e-26	-0.29	0.06		HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL
1476	1quu	A	480	749	6e-24	-0.02	0.54		HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL
1476	1quu	A	528	790	1.5e-24	0.07	0.21		HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL
1476	1ses	A	464	555	0.00017	-0.07	0.12		LIGASE(SYNTHETASE) SERYL-TRNA SYNTHETASE (EC 6.1.1.10) (SERINE-TRNA LIGASE) ISES 3 COMPLEXED WITH SERYL-HYDROXYAMATE-AMP ISES 4	CONTRACTILE PROTEIN
1479	1d44	A	609	667	0.00015	0.62	0.82		NEURO-ONCOLOGICAL VENTRAL ANTIGEN 1; CHAIN: A;	IMMUNE SYSTEM KH DOMAIN, ALPHA-BETA FOLD, RNA-BINDING MOTIF
1479	1d4j	A	609	667	0.00075	0.19	0.96		RNA-BINDING	IMMUNE SYSTEM KH DOMAIN,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									NEUROONCOLOGICAL VENTRAL ANTIGEN 2; CHAIN: A, B, C, D;	ALPHA-BETA FOLD RNA-BINDING MOTIF
1479	1dij	C	609	667	3e-06	0.59	0.94		RNA-BINDING NEUROONCOLOGICAL VENTRAL ANTIGEN 2; CHAIN: A, B, C, D;	IMMUNE SYSTEM KH DOMAIN, ALPHA-BETA FOLD RNA-BINDING MOTIF
1479	1ddj	D	609	667	1e-05	0.60	0.89		RNA-BINDING NEUROONCOLOGICAL VENTRAL ANTIGEN 2; CHAIN: A, B, C, D;	IMMUNE SYSTEM KH DOMAIN, ALPHA-BETA FOLD RNA-BINDING MOTIF
1479	1c3h	A	51	613	0	0.75	1.00		GUANOSINE PENTAPHOSPHATE SYNTHETASE; CHAIN: A;	POLYRIBONUCLEOTIDE TRANSFERASE POLYNUCLEOTIDE PHOSPHORYLASE, GUANOSINE POLYRIBONUCLEOTIDE TRANSFERASE, ATP-GTP 2 DIPHOSPHOTRANSFERASE, RNA PROCESSING, RNA DEGRADATION
1479	1c3p	A	51	739	0	0.49	1.00		GUANOSINE PENTAPHOSPHATE SYNTHETASE; CHAIN: A;	POLYRIBONUCLEOTIDE TRANSFERASE POLYNUCLEOTIDE PHOSPHORYLASE, GUANOSINE POLYRIBONUCLEOTIDE TRANSFERASE, ATP-GTP DIPHOSPHOTRANSFERASE, 2 RNA PROCESSING, RNA DEGRADATION
1479	1cc6	A	609	675	0.00014	0.50	0.72		RNA-BINDING PROTEIN NOVA-2; CHAIN: A, B; 20-MER RNA HAIRPIN; CHAIN: C, D;	RNA BINDING PROTEIN/NOVA-2; CYTIC NOVA-LIKE RNA-BINDING PROTEIN; KH DOMAIN, ALPHA-BETA FOLD, RNA-BINDING MOTIF, PROTEIN/NOVA 2 STRUCTURE
1479	1lkm	A	610	671	0.0014	0.56	0.56		HNRP K; CHAIN: A;	RNA BINDING PROTEIN KH3; HNRP K, KH DOMAIN, THREE-DIMENSIONAL STRUCTURE, NMR

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
										C-MYC, 2 DIPOLAR COUPLING, DNA-BINDING, RNA-BINDING, RNA BINDING, 3 PROTEIN
1479	1aro		675	751	5.1e-21	0.78	1.00		PNPASE; CHAIN: NULL;	SI RNA-BINDING DOMAIN POLYRIBONUCLEOTIDE NUCLEOTIDYLTRANSFERASE, SI RNA-BINDING DOMAIN, POLYNUCLEOTIDE PHOSPHORYLASE 2 (PNPASE) RIBONUCLEOPROTEIN RNA-BINDING PROTEIN IVIG 19
1479	1vig		603	667	1e-06	0.46	0.30		VIGILIN; IVIG 5 CHAIN: NULL; IVIG 6	
1480	1o9x	A	442	528	1.7e-06	-0.14	0.00		EXCINUCLEASE UVRABC COMPONENT UVRB; CHAIN: A;	GENE REGULATION APO PROTEIN
1480	1o9x	A	447	602	0.009	-0.21	0.03		EXCINUCLEASE UVRABC COMPONENT UVRB; CHAIN: A;	GENE REGULATION APO PROTEIN
1480	1fin	A	427	492	0.00015	-0.14	0.54		CELL DIVISION CONTROL PROTEIN 6; CHAIN: A, B;	CELL CYCLE CDC6P, CDC6, CDC18, ORC1, AAA PROTEIN, DNA REPLICATION INITIATION 2 FACTOR, CELL CYCLE CONTROL FACTOR
1480	1qhg	A	444	524	1.5e-11	-0.19	0.83		PCRA (SUBUNIT); CHAIN: A; PCRA (SUBUNIT); CHAIN: B; PCRA (SUBUNIT); CHAIN: C; PCRA (SUBUNIT); CHAIN: D;	HELICASE DNA REPAIR, DNA REPLICATION, SOS RESPONSE, HELICASE, ATP-2 BINDING, DNA-BINDING
1484	1aau		4	122	6.8e-26	0.28	0.96		T-FIMBRIN; CHAIN: NULL;	ACTIN-BINDING PROTEIN ACTIN-BINDING, PHOSPHORYLATION
1484	1dxx	A	2	120	5.1e-28	0.54	0.68		DYSTROPHIN; CHAIN: A, B, C, D;	STRUCTURAL PROTEIN DYSTROPHIN, MUSCULAR DYSTROPHY, CALPONIN HOMOLOG DOMAIN, 2 ACTIN-BINDING, UTROPHIN

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1484	1qag	A	5	121	3.4e-26	0.33	0.39		UTROPHIN ACTIN BINDING REGION; CHAIN: A, B;	STRUCTURAL, PROTEIN CALPONIN HOMOLOG DOMAIN, DOMAIN SWAPPING, ACTIN BINDING, 2 UTROPHIN, DYSTROPHIN, STRUCTURAL, PROTEIN
1486	1tt6	A	866	953	0.0045	-0.10	0.01		TFIIIA; CHAIN: A, D, 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 FINGER PROTEIN
1486	2gii	A	873	926	0.00045	0.08	0.41		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1487	1boc		339	377	0.0001	-0.38	0.00		TRANSCRIPTION FACTOR PML; CHAIN: NULL;	TRANSCRIPTION REGULATION PROTO-ONCOGENE, NUCLEAR BODIES (PODS), LEUKEMIA, 2 TRANSCRIPTION REGULATION
1487	1che		336	378	3.4e-10	-0.35	0.29		VIRUS EQUINE HERPES VIRUS-1 (C3HC4, OR RING DOMAIN) 1CHC 3 (NMR, 1 STRUCTURE) 1CHC 4	
1487	1bw	A	336	381	5.1e-09	-0.24	0.15		SIGNAL TRANSDUCTION PROTEIN CBL; CHAIN: A; ZAP-70 PEPTIDE; CHAIN: B; UBIQUITIN-CONJUGATING ENZYME E2-18 KDA UBECH7; CHAIN: C	LIGASE CBL, UBECH7, ZAP-70, E2, UBIQUITIN, E3, PHOSPHORYLATION, 2 TYROSINE KINASE, UBIQUITINATION, PROTEIN DEGRADATION,
1487	1g25	A	336	387	5.1e-06	0.26	0.62		CDK-ACTIVATING KINASE ASSEMBLY FACTOR MAT1;	METAL BINDING PROTEIN RING FINGER PROTEIN MAT1; RING

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1487	1rmd		320	387	3.4e-09	0.10	0.06		CHAIN: A; RAG1; CHAIN: NULL;	FINGER (C3HC4) DNA-BINDING PROTEIN V(DJ) RECOMBINATION ACTIVATING PROTEIN 1; RAG1, V(DJ) RECOMBINATION, ANTIODY, MAD, RING FINGER, 2 ZINC BINUCLEAR CLUSTER, ZINC FINGER, DNA-BINDING PROTEIN
1490	1d2n	A	626	782	1.2e-11	0.11	-0.18		N-ETHYLMALIMIDE- SENSITIVE FUSION PROTEIN; CHAIN: A;	HEXAMERIZATION DOMAIN HEXAMERIZATION DOMAIN, ATPASE, TRANSPORT
1490	1e94	E	339	434	8.5e-12	0.01	-0.13		HEAT SHOCK PROTEIN HSLV; CHAIN: A, B, C, D; HEAT SHOCK PROTEIN HSLU; CHAIN: E, F;	CHAPERONE HSLV; HSLU CHAPERONE, HSLV, CLPQY, AAA- ATPASE, ATP-DEPENDENT 2 PROTEOLYSIS, PROTEASOME
1490	1e94	E	339	634	1.5e-12	-0.20	0.05		HEAT SHOCK PROTEIN HSLV; CHAIN: A, B, C, D; HEAT SHOCK PROTEIN HSLU; CHAIN: E, F;	CHAPERONE HSLV; HSLU CHAPERONE, HSLV, CLPQY, AAA- ATPASE, ATP-DEPENDENT 2 PROTEOLYSIS, PROTEASOME
1490	1f48	A	82	514	0.0015	-0.39	0.28		ARSENITE-TRANSLOCATING ATPASE; CHAIN: A;	HYDROLASE ARSA ATPASE, P- LOOP, ANTIMONITE BINDING SITE, ATP BINDING SITE
1490	1fnn	A	344	629	1.2e-15	0.15	0.45		CELL DIVISION CONTROL PROTEIN 6; CHAIN: A, B;	CELL CYCLE CDC6, CDC18, ORC1, AAA PROTEIN, DNA REPLICATION INITIATION 2 FACTOR, CELL CYCLE CONTROL FACTOR
1490	1g41	A	330	599	1.2e-37	0.46	0.94		HEAT SHOCK PROTEIN HSLU; CHAIN: A;	CHAPERONE AAA-ATPASE, CLPQY, ATP-DEPENDENT PROTEOLYSIS
1490	1g41	A	339	618	1.2e-17	-0.11	0.04		HEAT SHOCK PROTEIN HSLU; CHAIN: A;	CHAPERONE AAA-ATPASE, CLPQY, ATP-DEPENDENT PROTEOLYSIS
1490	1shk	A	369	396	1.5e-05	-0.53	0.49		SHIKIMATE KINASE; CHAIN: A, B;	TRANSFERASE SHIKIMATE KINASE, PHOSPHORYL TRANSFER, ADP,

SEQ NO:	PDB ID	CHAIN ID	STAR T/AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1490	2fhf	A	347	537	1e-05	-0.24	0.01		PFH; CHAIN: A, B, C;	SHIKIMATE 2 PATHWAY, P-LOOP PROTEIN, TRANSFERASE
										PROTEIN TRANSPORT FIFTY-FOUR HOMOLOG, P45; PFH, SRP54, SIGNAL RECOGNITION PARTICLE, GTPASE, M DOMAIN, 2 RNA-BINDING, SIGNAL SEQUENCE-BINDING, HELIX-TURN-HELIX, 3 PROTEIN TARGETING, PROTEIN TRANSPORT
1491	1e4y	A	178	394	1.5e-48	0.10	0.94		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS
1491	1yrg	A	178	391	6.8e-27	0.03	0.18		GTPASE-ACTIVATING PROTEIN RNAI_SCHPO; CHAIN: A, B;	TRANSCRIPTION RNAI; RANGAP; GTPASE-ACTIVATING PROTEIN FOR SPT, GTPASE-ACTIVATING PROTEIN, GAP, RNAI, RANGAP, LRR, LEUCINE-2 RICH REPEAT PROTEIN, TWINNING, HEMIHEDRAL TWINNING, 3 MEROHEDRAL TWINNING, MEROHEDRY
1491	2bnh		178	393	3.4e-43	0.33	0.65		RIBONUCLEASE INHIBITOR; CHAIN: NULL;	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS
1495	1lit		36	166	1e-42	0.82	1.00		LITHOSTATHINE; CHAIN: NULL	PANCREATIC STONE INHIBITOR, PANCREATIC STONE INHIBITOR, LECTIN

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1495	1lit		36	166	7.5e-43	0.82	1.00		LITHOSTATHINE; CHAIN: NULL	PANCREATIC STONE INHIBITOR PANCREATIC STONE INHIBITOR, LECTIN
1495	1lit		36	166	7.5e-43			212.11	LITHOSTATHINE; CHAIN: NULL	PANCREATIC STONE INHIBITOR PANCREATIC STONE INHIBITOR, LECTIN
1495	1qdd	A	23	166	1e-44	0.77	1.00		LITHOSTATHINE; CHAIN: A;	METAL BINDING PROTEIN PANCREATIC STONE PROTEIN, PSP; PANCREATIC STONE INHIBITOR, LITHOSTATHINE
1495	1qdd	A	23	166	6e-47	0.77	1.00		LITHOSTATHINE; CHAIN: A;	METAL BINDING PROTEIN PANCREATIC STONE PROTEIN, PSP; PANCREATIC STONE INHIBITOR, LITHOSTATHINE
1495	1qdd	A	23	166	6e-47			226.04	LITHOSTATHINE; CHAIN: A;	METAL BINDING PROTEIN PANCREATIC STONE PROTEIN, PSP; PANCREATIC STONE INHIBITOR, LITHOSTATHINE
1497	1qqe	A	489	634	1.1e-13	0.14	-0.17		VESICULAR TRANSPORT PROTEIN SEC17; CHAIN: A;	PROTEIN TRANSPORT HELIX- TURN-HELIX TPR-LIKE REPEAT, PROTEIN TRANSPORT
1498	1eul	A	1	713	0	-0.16	0.46		CALCIUM-TRANSPORTING ATPASE SARCOPLASMIC CHAIN: A;	HYDROLASE SERCA1; ION PUMP, CALCIUM MEMBRANE PROTEIN, P- TYPE ATPASE, ACTIVE 2 TRANSPORT
1499	1e4o	A	393	540	1e-12	0.20	0.96		DNA NUCLEOTIDE EXCISION REPAIR ENZYME UVRB; CHAIN: A;	REPLICATION DNA NUCLEOTIDE EXCISION REPAIR, UVRABC, HELICASE, 2
1499	1e4o	A	448	516	1.4e-19	-0.10	0.83		DNA NUCLEOTIDE EXCISION REPAIR ENZYME UVRB;	HYPER-THERMOSTABLE PROTEIN REPLICATION DNA NUCLEOTIDE EXCISION REPAIR, UVRABC,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1499	1d2m	A	144	223	0.00068	-0.57	0.19		CHAIN: A;	HELICASE, 2
1499	1d2m	A	393	540	8.5e-13	0.17	0.80		EXCINUCLEASE ABC SUBUNIT B; CHAIN: A;	HYPERTHERMOSTABLE PROTEIN
1499	1d9x	A	258	531	9e-29	-0.16	0.09		EXCINUCLEASE ABC SUBUNIT B; CHAIN: A;	HYDROLASE UVRB; MULTIDOMAIN PROTEIN
1499	1d9x	A	380	528	3.4e-16	0.39	0.76		EXCINUCLEASE UVRA3 COMPONENT UVRB; CHAIN: A;	GENE REGULATION APO PROTEIN
1499	1f1k	A	376	558	1.2e-43	0.26	0.86		EXCINUCLEASE UVRA3 COMPONENT UVRB; CHAIN: A;	GENE REGULATION APO PROTEIN
1499	1flu	A	127	340	3.4e-59	0.83	1.00		YEAST INITIATION FACTOR 4A; CHAIN: A, B;	TRANSLATION YEAST INITIATION FACTOR 4A, IF4A; HELICASE, INITIATION FACTOR 4A, DEAD-BOX PROTEIN
1499	1flu	B	127	558	0	0.47	1.00		YEAST INITIATION FACTOR 4A; CHAIN: A, B;	TRANSLATION EUKARYOTIC INITIATION FACTOR 4A; IF4A, HELICASE, DEAD-BOX PROTEIN
1499	1hei	A	158	325	0.0003	-0.18	0.22		HCV HELICASE; CHAIN: A, B;	HEPATITIS, HCV, ATPASE, NTPASE
1499	1qde	A	127	340	5.1e-56	0.55	1.00		TRANSLATION INITIATION FACTOR 4A; CHAIN: A;	GENE REGULATION IF4A; TRANSLATION INITIATION, SACCHAROMYCES CEREVISIAE, DEAD BOX 2 PROTEIN FAMILY
1499	8ohm		158	522	1.5e-53	-0.59	0.04		RNA HELICASE; CHAIN: NULL	HELICASE RNA HELICASE, HEPATITIS C VIRUS, HCV, UNWINDING MECHANISM
1502	1a25	A	12	137	9e-25			77.04	PROTEIN KINASE C (BETA); CHAIN: A, B;	CALCIUM-BINDING PROTEIN CALB; CALCIUM(II)-PHOSPHOLIPID BINDING PROTEIN; 2 CALCIUM-BINDING PROTEIN

SEQ NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1502	1a25	A	167	287	1.5e-26	-0.05	0.54		PROTEIN KINASE C (BETA); CHAIN: A, B;	CALCIUM-BINDING PROTEIN CALB; CALCIUM-H+PHOSPHOLIPID BINDING PROTEIN, 2 CALCIUM-BINDING PROTEIN
1502	1a25	A	17	131	9e-25	0.42	1.00		PROTEIN KINASE C (BETA); CHAIN: A, B;	CALCIUM-BINDING PROTEIN CALB; CALCIUM-H+PHOSPHOLIPID BINDING PROTEIN, 2 CALCIUM-BINDING PROTEIN
1502	1a25	A	18	117	1.4e-24	0.62	0.90		PROTEIN KINASE C (BETA); CHAIN: A, B;	CALCIUM-BINDING PROTEIN CALB; CALCIUM-H+PHOSPHOLIPID BINDING PROTEIN, 2 CALCIUM-BINDING PROTEIN
1502	1byn	A	167	287	3.4e-30	0.04	0.35		SYNAPTOTAGMIN I; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN, C2-DOMAIN, EXOCYTOSIS, NEUROTRANSMITTER 2 RELEASE, ENDOCYTOSIS/EXOCYTOSIS
1502	1byn	A	19	122	1.7e-28	0.36	0.10		SYNAPTOTAGMIN I; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN, C2-DOMAIN, EXOCYTOSIS, NEUROTRANSMITTER 2 RELEASE, ENDOCYTOSIS/EXOCYTOSIS
1502	1c1j	A	184	338	1.3e-29	0.07	0.65		CYTOSOLIC PHOSPHOLIPASE A2; CHAIN: A, B;	HYDROLASE CPLA2; PHOSPHOLIPASE, LIPID-BINDING, HYDROLASE
1502	1c1j	A	22	184	7.5e-24	0.29	0.45		CYTOSOLIC PHOSPHOLIPASE A2; CHAIN: A, B;	HYDROLASE CPLA2; PHOSPHOLIPASE, LIPID-BINDING, HYDROLASE
1502	1c1j	A	183	302	3.4e-22	0.34	0.24		PHOSPHONOSITIDE-SPECIFIC PHOSPHOLIPASE C; CHAIN: A, B;	LIPID DEGRADATION PLC-D1; PHOSPHORIC DIESTER HYDROLASE, HYDROLASE, LIPID DEGRADATION, 2 TRANSDUCER, CALCIUM-BINDING, PHOSPHOLIPASE C, 3

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fsl Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1502	1dix	A	27	121	6.8e-23	0.49	0.16		PHOSPHOINOSITIDE-SPECIFIC PHOSPHOLIPASE C, CHAIN: A, B;	PHOSPHOINOSITIDE-SPECIFIC LIPID DEGRADATION PLC-D1; PHOSPHORIC DIESTER HYDROLASE, LIPID DEGRADATION, 2 TRANSDUCER, CALCIUM-BINDING, PHOSPHOLIPASE C, 3
1502	1dix	B	183	302	3.4e-22	0.20	0.21		PHOSPHOINOSITIDE-SPECIFIC PHOSPHOLIPASE C, CHAIN: A, B;	PHOSPHOINOSITIDE-SPECIFIC LIPID DEGRADATION PLC-D1; PHOSPHORIC DIESTER HYDROLASE, LIPID DEGRADATION, 2 TRANSDUCER, CALCIUM-BINDING, PHOSPHOLIPASE C, 3
1502	1day	A	17	137	1e-24	0.52	1.00		PROTEIN KINASE C, ALPHA TYPE; CHAIN: A;	TRANSFERASE CALCIUM++; PHOSPHOLIPID BINDING PROTEIN, CALCIUM-BINDING 2 PROTEIN, PHOSPHATIDYL SERINE, PROTEIN KINASE C
1502	1day	A	183	295	5.1e-28	-0.13	0.07		PROTEIN KINASE C, ALPHA TYPE; CHAIN: A;	TRANSFERASE CALCIUM++; PHOSPHOLIPID BINDING PROTEIN, CALCIUM-BINDING 2 PROTEIN, PHOSPHATIDYL SERINE, PROTEIN KINASE C
1502	1day	A	18	117	6.8e-27	0.47	0.88		PROTEIN KINASE C, ALPHA TYPE; CHAIN: A;	TRANSFERASE CALCIUM++; PHOSPHOLIPID BINDING PROTEIN, CALCIUM-BINDING 2 PROTEIN, PHOSPHATIDYL SERINE, PROTEIN KINASE C
1502	1rlw		184	276	6e-23	0.17	0.28		PHOSPHOLIPASE A2; CHAIN: NULL;	HYDROLASE CALB DOMAIN; HYDROLASE, C2 DOMAIN, CALB DOMAIN
1502	1rlw		20	145	4.5e-25			51.76	PHOSPHOLIPASE A2; CHAIN:	HYDROLASE CALB DOMAIN;

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Fsi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1502	1rlw		30	143	4.5e-25	0.78	0.93		NULL;	HYDROLASE, C2 DOMAIN, CALB DOMAIN
1502	1rsy		167	284	3.4e-30	0.18	0.48		PHOSPHOLIPASE A2; CHAIN: NULL;	HYDROLASE CALB DOMAIN; HYDROLASE, C2 DOMAIN, CALB DOMAIN
1502	1rsy		19	122	1.7e-28	0.36	0.21		CALCIUM/PHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN I (FIRST C2 DOMAIN) (CALB) IRSY 3	
1502	1rsy		2	130	1.7e-28			59.11	CALCIUM/PHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN I (FIRST C2 DOMAIN) (CALB) IRSY 3	
1502	3rpb	A	168	294	1.2e-26	0.00	0.34		BINDING PROTEIN SYNAPTOTAGMIN I (FIRST C2 DOMAIN) (CALB) IRSY 3 RABPHILIN 3-A; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS C2- DOMAINS, C2B-DOMAIN, RABPHILIN, ENDOCYTOSIS/EXOCYTOSIS ENDOCYTOSIS/EXOCYTOSIS BETA SANDWICH, CALCIUM ION, C2 DOMAIN
1502			144	223	6.8e-53	-0.57	0.19		SYNAPTOTAGMIN III; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS ENDOCYTOSIS/EXOCYTOSIS ENDOCYTOSIS/EXOCYTOSIS BETA SANDWICH, CALCIUM ION, C2 DOMAIN
1503	lawe	B	693	861	1.5e-26	0.40	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA I; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABP ALPHA; GABP BETA I; COMPLEX (TRANSCRIPTION REGULATION/DNA) DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANK YRIN REPEATS, TRANSCRIPTION 3 FACTOR COMPLEX (TRANSCRIPTION
1503	lawe	B	694	828	1.2e-29	0.29	0.96		GA BINDING PROTEIN ALPHA;	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	REGULATION(DNA) GABPALPHA; GABPETA1; COMPLEX (TRANSCRIPTION REGULATION(DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1503	lawc	B	748	895	5.1e-38	0.68	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION(DNA) GABPALPHA; GABPETA1; COMPLEX (TRANSCRIPTION REGULATION(DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1503	lawc	B	779	936	7.5e-34	0.72	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION(DNA) GABPALPHA; GABPETA1; COMPLEX (TRANSCRIPTION REGULATION(DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1503	lawc	B	780	970	1.2e-31	0.02	0.78		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION(DNA) GABPALPHA; GABPETA1; COMPLEX (TRANSCRIPTION REGULATION(DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1503	lawc	B	847	1005	3.4e-29	0.08	-0.11		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B;	COMPLEX (TRANSCRIPTION REGULATION(DNA) GABPALPHA; GABPETA1; COMPLEX

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									DNA; CHAIN: D, E;	(TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ET'S DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1503	1awc	B	880	1045	1.7e-29	0.05	-0.11		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABP/ALPHA; GABP/BETA 1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ET'S DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1503	1bd8		697	862	3.4e-26	0.26	0.98		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1503	1bd8		776	937	4.5e-32	0.60	1.00		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1503	1bix	B	695	868	1.1e-26	0.37	0.99		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1503	1bix	B	697	862	1.4e-24	0.07	0.76		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1503	1bix	B	779	941	7.5e-33	0.64	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT

SEQ ID NO:	PDB ID	CHAIN ID	STAR T A A	END A A	Psi Blast	Verify score	FMF score	SEQFOL D score	Compound	PDB annotation
										KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1503	1bu9	A	697	867	3.4e-31	0.42	0.84		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
1503	1bu9	A	748	894	6.8e-32	0.39	0.99		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
1503	1d9e	A	693	833	3e-19	0.23	0.77		CYCLIN-DEPENDENT KINASE 4 INHIBITOR B; CHAIN: A;	SIGNALING PROTEIN HELIX-TURN-HELIX, ANKYRIN REPEAT
1503	1d9e	A	776	909	1.2e-32	0.81	1.00		CYCLIN-DEPENDENT KINASE 4 INHIBITOR B; CHAIN: A;	SIGNALING PROTEIN HELIX-TURN-HELIX, ANKYRIN REPEAT
1503	1d9q	A	685	881	1.4e-21	-0.07	0.65		PK2-ASSOCIATED PROTEIN BETA; CHAIN: A;	METAL BINDING PROTEIN ZINC-BINDING MODULE, ANKYRIN REPEATS, METAL BINDING PROTEIN
1503	1lib	A	697	866	1.7e-30	0.22	1.00		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
1503	1lib	A	748	894	6.8e-32	0.52	1.00		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
1503	1lkn	D	640	812	1.7e-31	0.21	0.31		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-	TRANSCRIPTION FACTOR P65, P50D, TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1503	1lkn	D	693	912	3e-34	0.10	1.00		B-ALPHA; CHAIN: D; NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; IKAPPA- B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
1503	1lkn	D	722	882	3.4e-38	0.37	1.00		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; IKAPPA- B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
1503	1lkn	D	747	947	3e-41	0.52	1.00		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; IKAPPA- B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
1503	1lkn	D	776	983	3e-38	0.37	1.00		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; IKAPPA- B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
1503	1nfi	E	640	812	1.7e-31	0.15	0.88		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; IKAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1503	1nfi	E	693	909	7.5e-34	0.43	1.00		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; IKAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1503	1nfi	E	721	882	8.5e-38	0.42	1.00		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; IKAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1503	1nfi	E	776	982	3e-35	0.50	1.00		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX

SEQ NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									1-KAPPA-B-ALPHA; CHAIN: E, F;	(TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1504	1a26		958	1128	1e-35	0.01	0.52		POLY (ADP-RIBOSE) POLYMERASE; CHAIN: NULL;	TRANSFERASE PARP-CF, POLY (ADP-RIBOSE) TRANSFERASE, POLY TRANSFERASE, GLYCOSYLTRANSFERASE, NAD(+) 2 ADP-RIBOSYLTRANSFERASE
1504	1a26		994	1127	1.7e-08	-0.24	0.16		POLY (ADP-RIBOSE) POLYMERASE; CHAIN: NULL;	TRANSFERASE PARP-CF, POLY (ADP-RIBOSE) TRANSFERASE, GLYCOSYLTRANSFERASE, NAD(+) 2 ADP-RIBOSYLTRANSFERASE
1504	1awc	B	128	296	3.4e-35	0.46	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA I; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1504	1awc	B	185	329	6.8e-39	0.22	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA I; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1504	1awc	B	215	357	1.7e-36	0.15	0.86		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA I; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
										REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1504	lawc	B	25	164	3e-43	0.62	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA I; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABP ALPHA; GABP BETA I; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1504	lawc	B	26	176	1.5e-39	0.75	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA I; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABP ALPHA; GABP BETA I; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1504	lawc	B	335	482	1.2e-33	0.69	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA I; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABP ALPHA; GABP BETA I; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1504	lawc	B	402	578	1.2e-37	0.17	0.95		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA I; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABP ALPHA; GABP BETA I; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR

SEQ NO:	PDB ID	CILAI N ID	STAR T AA	END AA	Fsi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1504	lawc	B	437	611	3.4e-33	0.04	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR, COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1504	lawc	B	491	644	4.5e-47	0.49	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1504	lawc	B	491	644	4.5e-47			105.28	GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1504	lawc	B	496	640	8.5e-39	0.47	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1504	1awe	B	645	784	3e-42	0.64	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1504	1awe	B	660	797	3.4e-38	0.49	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1504	1awe	B	683	817	1.2e-35	0.28	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1504	1awe	B	89	296	1.4e-40	-0.00	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1504	1b0x	A	877	933	9e-07	1.27	1.00		EPHA4 RECEPTOR TYROSINE KINASE; CHAIN: A;	TRANSPERASE RECEPTOR TYROSINE KINASE, PROTEIN

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	FMF score	SEQFOL D score	Compound	PDB annotation
										INTERACTION MODULE, 2 DIMERIZATION DOMAIN, TRANSFERASE
1504	1b0x	A	877	941	3.4e-06	1.08	1.00		EPHA4 RECEPTOR TYROSINE KINASE, CHAIN: A;	TRANSFERASE RECEPTOR TYROSINE KINASE, PROTEIN INTERACTION MODULE, 2 DIMERIZATION DOMAIN, TRANSFERASE
1504	1b4f	A	875	935	0.00014	0.82	0.99		EPHB2; CHAIN: A, B, C, D, E, F, G, H;	SIGNAL TRANSDUCTION SAM DOMAIN, EPB RECEPTOR, SIGNAL TRANSDUCTION, OLIGOMER
1504	1b4f	A	877	933	4.5e-10	0.72	0.99		EPHB2; CHAIN: A, B, C, D, E, F, G, H;	SIGNAL TRANSDUCTION SAM DOMAIN, EPB RECEPTOR, SIGNAL TRANSDUCTION, OLIGOMER
1504	1bd8		179	317	4.3e-36	0.43	1.00		P19NK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1504	1bd8		24	164	3e-39	0.67	1.00		P19NK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1504	1bd8		332	483	1e-28	0.67	1.00		P19NK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1504	1bd8		402	581	3e-34	0.13	0.98		P19NK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1504	1bd8		433	614	7.5e-39	0.14	1.00		P19NK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1504	1bd8		492	643	1.5e-42	0.82	1.00		P19NK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1504	1bd8		525	701	1.5e-41	0.09	1.00		P19NK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR,

SEQ ID NO:	PDB ID	CHAI ID	STAR T AA	END AA	Fs Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1504	1bd8		594	767	6e-41	0.31	1.00		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	ANKYRIN MOTIF TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1504	1bd8		62	266	4.5e-39	0.09	0.94		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1504	1bd8		644	784	3e-41	0.50	1.00		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1504	1bd8		660	800	1e-28	0.51	1.00		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1504	1bd8		683	818	1.4e-28	0.47	0.99		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1504	1bd8		95	299	1.2e-37	-0.32	0.53		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1504	1bbx	B	179	317	1.5e-35	0.45	1.00		CYCCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1504	1bbx	B	248	459	1.2e-31	-0.31	0.01		CYCCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1504	1bbx	B	26	164	1.5e-39	0.60	1.00		CYCCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fsi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1504	1bix	B	332	483	4.5e-30	0.49	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1504	1bix	B	435	618	1.5e-41	0.34	0.99		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1504	1bix	B	494	643	7.5e-42	0.72	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1504	1bix	B	594	771	4.5e-45	0.17	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1504	1bix	B	648	784	9e-40	0.59	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1504	1bix	B	660	800	8.5e-28	0.54	1.00		CYCLIN-DEPENDENT KINASE	COMPLEX (INHIBITOR

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Ts Blast	Verify score	PMF score	SEQ/FOL D score	Compound	PDB annotation
									6; CHAIN: A; P19INK4D; CHAIN: B;	PROTEIN(KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1504	1bix	B	683	818	1.4e-28	0.30	0.99		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1504	1bu9	A	182	334	1.7e-36	0.28	0.92		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
1504	1bu9	A	28	176	1.2e-33	0.85	1.00		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
1504	1bu9	A	496	640	1.4e-32	0.64	1.00		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
1504	1bu9	A	663	802	5.1e-33	0.37	1.00		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
1504	1d9e	A	485	617	6e-35	0.63	1.00		CYCLIN-DEPENDENT KINASE 4 INHIBITOR B; CHAIN: A;	SIGNALING PROTEIN HELIX-TURN-HELIX, ANKYRIN REPEAT
1504	1d9e	A	49	164	3e-35	0.27	1.00		CYCLIN-DEPENDENT KINASE	SIGNALING PROTEIN HELIX-TURN-HELIX, ANKYRIN REPEAT

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1504	1c9s	A	517	643	7.5e-38	0.32	1.00		4 INHIBITOR B; CHAIN: A; CYCLIN-DEPENDENT KINASE	HELIX, ANKYRIN REPEAT
1504	1c9s	A	585	770	6e-37	0.17	0.45		4 INHIBITOR B; CHAIN: A; CYCLIN-DEPENDENT KINASE	SIGNALING PROTEIN HELIX-TURN-HELIX, ANKYRIN REPEAT
1504	11hb	A	182	333	8.5e-36	0.40	1.00		4 INHIBITOR B; CHAIN: A; CYCLIN-DEPENDENT KINASE	SIGNALING PROTEIN HELIX-TURN-HELIX, ANKYRIN REPEAT
									6 INHIBITOR; CHAIN: A, B; CYCLIN-DEPENDENT KINASE	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
1504	11hb	A	28	176	1.2e-35	0.84	1.00		CYCLIN-DEPENDENT KINASE	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
1504	11hb	A	496	640	1.4e-32	0.68	1.00		6 INHIBITOR; CHAIN: A, B; CYCLIN-DEPENDENT KINASE	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
1504	11hb	A	663	801	1.7e-32	0.47	1.00		6 INHIBITOR; CHAIN: A, B; CYCLIN-DEPENDENT KINASE	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
1504	11kn	D	156	366	1.2e-35	-0.18	0.00		NE-KAPPA-B P65 SUBUNIT; CHAIN: A; NE-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKBNFKB COMPLEX
1504	11kn	D	210	403	1.7e-33	-0.38	0.30		NE-KAPPA-B P65 SUBUNIT; CHAIN: A; NE-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKBNFKB COMPLEX
1504	11kn	D	28	240	1.5e-48	0.36	1.00		NE-KAPPA-B P65 SUBUNIT;	TRANSCRIPTION FACTOR P65;

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D;	P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
1504	1lik	D	399	562	1.4e-30	-0.26	0.30		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
1504	1lik	D	525	715	5.1e-34	-0.26	0.06		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
1504	1lik	D	528	775	6e-60	-0.05	0.55		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
1504	1lik	D	558	748	1.7e-36	-0.36	0.25		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
1504	1lik	D	672	817	1.7e-36	0.20	0.92		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
1504	1lik	D	90	296	8.5e-40	-0.05	0.80		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
1504	1lik	D	91	396	4.5e-40	-0.19	0.12		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
1504	1myo		213	317	3e-35	0.09	0.98		MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT
1504	1myo		365	482	6e-30	0.57	1.00		MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQOL D score	Compound	PDB annotation
1504	1myo		528	644	3e-39	0.51	1.00		MYOTROPHIN; CHAIN: NULL	ACETYLTATION, NMR, ANK-REPEAT
1504	1myo		61	165	1.3e-38	0.03	1.00		MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN, ACETYLTATION, NMR, ANK-REPEAT
1504	1myo		681	794	7.5e-39	0.66	1.00		MYOTROPHIN; CHAIN: NULL	ACETYLTATION, NMR, ANK-REPEAT
1504	1myo		684	799	6.8e-25	0.37	0.86		MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN, ACETYLTATION, NMR, ANK-REPEAT
1504	1inf	E	154	366	6.8e-36	-0.11	0.58		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; IKAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REG/ANK REPEAT), REGULATION/ANK REPEAT, ANKYRIN 2 REPEAT HELIX
1504	1inf	E	154	424	1.5e-40	-0.17	0.93		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; IKAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1504	1inf	E	208	458	1.2e-44	-0.34	0.36		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; IKAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1504	1inf	E	209	403	5.1e-33	-0.01	0.96		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; IKAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1504	1inf	E	365	622	1.5e-50	0.08	0.41		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; IKAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fst Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1304	1inf	E	429	643	3e-45	0.08	0.95		NE-KAPPA-B P65; CHAIN: A, C; NE-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E; F ₂	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION) REGULATION/ANK REPEAT, ANKYRIN 2 REPEAT HELIX
1504	1inf	E	463	628	5.1e-37	0.35	1.00		NE-KAPPA-B P65; CHAIN: A, C; NE-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E; F ₂	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION) REGULATION/ANK REPEAT, ANKYRIN 2 REPEAT HELIX
1504	1inf	E	490	682	1.7e-32	0.34	0.99		NE-KAPPA-B P65; CHAIN: A, C; NE-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E; F ₂	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION) REGULATION/ANK REPEAT, ANKYRIN 2 REPEAT HELIX
1304	1inf	E	528	777	6e-57	-0.06	1.00		NE-KAPPA-B P65; CHAIN: A, C; NE-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E; F ₂	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION) REGULATION/ANK REPEAT, ANKYRIN 2 REPEAT HELIX
1504	1inf	E	61	307	1.3e-54	-0.13	0.49		NE-KAPPA-B P65; CHAIN: A, C; NE-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E; F ₂	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION) REGULATION/ANK REPEAT, ANKYRIN 2 REPEAT HELIX
1304	1inf	E	672	817	1.7e-36	0.22	1.00		NE-KAPPA-B P65; CHAIN: A, C; NE-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E; F ₂	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION) REGULATION/ANK REPEAT, ANKYRIN 2 REPEAT HELIX
1504	1inf	E	88	296	6.8e-40	0.12	0.98		NE-KAPPA-B P65; CHAIN: A, C; NE-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E; F ₂	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION) REGULATION/ANK REPEAT,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1504	1agg		875	935	0.00034	0.65	0.84		EPHRIIN TYPE-B RECEPTOR 2; CHAIN: NULL;	ANKYRIN 2 REPEAT HELIX TYROSINE-PROTEIN KINASE NMR, RECEPTOR OLIGOMERIZATION, EPH RECEPTORS, TYROSINE 2 PHOSPHORYLATION, SIGNAL TRANSDUCTION, TYROSINE-PROTEIN 3 KINASE
1504	1agg		877	933	1.5e-09	0.78	0.59		EPHRIIN TYPE-B RECEPTOR 2; CHAIN: NULL;	TYROSINE-PROTEIN KINASE NMR, RECEPTOR OLIGOMERIZATION, EPH RECEPTORS, TYROSINE 2 PHOSPHORYLATION, SIGNAL TRANSDUCTION, TYROSINE-PROTEIN 3 KINASE
1504	1aw6	A	527	784	6e-37	-0.22	0.18		REGULATORY PROTEIN SWI6; CHAIN: A, B;	TRANSCRIPTION REGULATION, TRANSCRIPTION REGULATION, ANKYRIN REPEATS, CELL-CYCLE
1504	1yes	B	366	569	6e-30	-0.13	0.84		P53; CHAIN: A; 53BP2; CHAIN: B;	COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS) P53BP2, ANKYRIN REPEATS, SH3, P53, TUMOR SUPPRESSOR, MULTIGENE 2 FAMILY, NUCLEAR PROTEIN, PHOSPHORYLATION, DISEASE MUTATION, 3 POLYMORPHISM, COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS)
1504	1yes	B	528	722	4.5e-40	-0.03	1.00		P53; CHAIN: A; 53BP2; CHAIN: B;	COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS) P53BP2, ANKYRIN REPEATS, SH3, P53, TUMOR SUPPRESSOR, MULTIGENE 2 FAMILY, NUCLEAR PROTEIN, PHOSPHORYLATION, DISEASE MUTATION, 3 POLYMORPHISM, COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS)

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1504	1yes	B	59	254	7.5e-39	0.01	0.76		P53; CHAIN: A; 53BP2; CHAIN: B;	COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS) PSBP2; ANKYRIN REPEATS, SH3, P53, TUMOR SUPPRESSOR, MULTIGENE 2 FAMILY, NUCLEAR PROTEIN, PHOSPHORYLATION, DISEASE MUTATION, 3 POLYMORPHISM, COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS)
1507	1a17		39	190	1.7e-29	-0.10	0.05		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	HYDROLASE TETRAPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE
1507	1bor		218	262	3e-14	-0.76	0.13		TRANSCRIPTION FACTOR PML; CHAIN: NULL;	TRANSCRIPTION REGULATION PROTO-ONCOGENE, NUCLEAR BODIES (PODS), LEUKEMIA, 2 TRANSCRIPTION REGULATION
1507	1che		221	262	6e-14	-0.25	0.82		VIRUS EQUINE HERPES VIRUS-1 (C3HC4, OR RING DOMAIN) 1CHC 3 (NMR, 1 STRUCTURE) 1CHC 4	
1507	1e96	B	40	191	3.4e-14	0.02	-0.03		RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 1; CHAIN: A; NEUTROPHIL CYTOSOL FACTOR 2 (NCF-2) CHAIN: B;	SIGNALLING COMPLEX RAC1; P67PHOX; SIGNALLING COMPLEX, GTPASE, NADPH OXIDASE, PROTEIN-PROTEIN 2 COMPLEX, TPR MOTIF
1507	1e1r	A	39	161	6.8e-22	0.05	0.31		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT; HSP90, 2 PROTEIN BINDING
1507	1e1w	A	24	110	1.5e-11	0.00	-0.02		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN:	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1507	1clw	A	39	153	1.4e-21	0.13	0.24		C, D; TPRI-DOMAIN OF HOP; CHAIN: A, B; HSC70/PEPTIDE; CHAIN: C, D; REPEAT, HSC70, 2 HSP70, PROTEIN BINDING	REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
1507	1g25	A	221	262	4.5e-13	-0.20	0.37		CDK-ACTIVATING KINASE ASSEMBLY FACTOR MAT1; CHAIN: A; METAL BINDING PROTEIN RING FINGER PROTEIN MAT1; RING FINGER (C3HC4)	CDK-ACTIVATING KINASE ASSEMBLY FACTOR MAT1; RING FINGER (C3HC4)
1507	1rmd		210	302	9e-17	0.13	0.84		RAG1; CHAIN: NULL; DNA-BINDING PROTEIN V(D)J RECOMBINATION ACTIVATING PROTEIN 1; RAG1, V(D)J RECOMBINATION, ANTIBODY, MAD, RING FINGER, 2 ZINC BINUCLEAR CLUSTER, ZINC FINGER, DNA-BINDING PROTEIN	DNA-BINDING PROTEIN V(D)J RECOMBINATION ACTIVATING PROTEIN 1; RAG1, V(D)J RECOMBINATION, ANTIBODY, MAD, RING FINGER, 2 ZINC BINUCLEAR CLUSTER, ZINC FINGER, DNA-BINDING PROTEIN
1508	1adq	L	352	551	8.5e-18	-0.07	0.64		IGGH REA; CHAIN: A; RE-AN IGM/LAMBDA; CHAIN: H, L; COMPLEX (IMMUNOGLOBULIN/AUTOANTIGEN) COMPLEX (IMMUNOGLOBULIN/AUTOANTIGEN), RHEUMATOID FACTOR 2 AUTO-ANTIBODY COMPLEX	COMPLEX (IMMUNOGLOBULIN/AUTOANTIGEN) COMPLEX (IMMUNOGLOBULIN/AUTOANTIGEN), RHEUMATOID FACTOR 2 AUTO-ANTIBODY COMPLEX
1508	1bth	A	262	628	5.1e-43	0.18	0.39		HEMOLIN; CHAIN: A, B; INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION
1508	1bth	A	350	721	1.5e-43	0.34	0.49		HEMOLIN; CHAIN: A, B; INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION
1508	1bth	A	449	812	1.7e-50	0.29	0.96		HEMOLIN; CHAIN: A, B; INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION
1508	1bth	A	450	813	1.7e-50			124.44	HEMOLIN; CHAIN: A, B; INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1508	1b1h	A	4	335	5.1e-37	0.00	-0.07		HEMOLIN; CHAIN: A, B;	HOMOPHILIC ADHESION
1508	1b1h	A	726	1073	6.8e-40	0.15	0.36		HEMOLIN; CHAIN: A, B;	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION
1508	1b1h	A	74	447	4.5e-37	0.06	0.49		HEMOLIN; CHAIN: A, B;	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION
1508	1b1h	A	816	1184	3.4e-46	0.18	0.21		HEMOLIN; CHAIN: A, B;	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION
1508	1cdy		557	723	1.5e-15	0.42	0.42		T-CELL SURFACE GLYCOPROTEIN CD4; CHAIN: NULL;	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION
1508	1cs6	A	178	535	8.5e-49	-0.05	0.53		AXONIN-1; CHAIN: A;	T-CELL SURFACE GLYCOPROTEIN
1508	1cs6	A	262	628	1.5e-49	0.07	0.41		AXONIN-1; CHAIN: A;	IMMUNOGLOBULIN FOLD, TRANSMEMBRANE,
1508	1cs6	A	348	721	5.1e-63	0.15	0.62		AXONIN-1; CHAIN: A;	GLYCOPROTEIN, T-CELL, 2 MHC, LIPOPROTEIN, T-CELL SURFACE
1508	1cs6	A	3	347	1e-44	0.08	-0.01		AXONIN-1; CHAIN: A;	GLYCOPROTEIN
1508	1cs6	A	449	813	3.4e-55	0.26	0.84		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
1508	1cs6	A	536	897	5.1e-49	0.24	0.70		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
1508	1cs6	A	64	448	6.8e-37	0.05	-0.08		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
1508	1cs6	A	74	448	7.5e-39	0.07	-0.02		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION

SEQ NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
1508	1es6	A	829	1185	8.5e-48	0.04	0.24		AXONIN-1; CHAIN: A;	ADHESION CELL ADHESION NEURAL CELL ADHESION
1508	1es5	C	1009	1184	1.7e-38	0.13	-0.01		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1508	1es5	C	1096	1260	5.1e-21	0.08	-0.19		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1508	1es5	C	178	346	6.8e-21	-0.16	0.30		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1508	1es5	C	2	146	3.4e-17	0.23	-0.15		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1508	1es5	C	361	535	5.1e-23	0.17	0.21		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1508	1es5	C	450	628	8.5e-38	-0.05	0.54		FIBROBLAST GROWTH	GROWTH FACTOR/GROWTH

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1508	1evs	C	61	260	5.1e-24	-0.10	0.27		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1508	1evs	C	642	812	8.5e-36	-0.42	0.21		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1508	1evs	C	737	896	1.7e-24	0.07	-0.05		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1508	1evs	C	813	996	1.7e-37	0.05	-0.15		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1508	1evs	D	1009	1184	5.1e-34	0.23	0.06		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR

SEQ NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1508	1evs	D	178	346	1.2e-21	-0.19	0.82		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	FACTOR RECEPTOR GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1508	1evs	D	271	447	1.7e-33	0.15	0.01		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1508	1evs	D	2	146	6.8e-19	0.19	-0.05		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1508	1evs	D	361	535	8.5e-25	0.19	0.25		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1508	1evs	D	450	628	3.4e-35	-0.02	0.71		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1508	1evs	D	61	260	1.2e-22	0.13	0.30		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									FACTOR RECEPTOR 1; CHAIN: C, D;	TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1508	1evs	D	642	812	1.2e-36	-0.31	0.00		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR GGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1508	1evs	D	737	896	1.7e-25	0.11	0.04		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR GGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1508	1evs	D	813	996	3.4e-34	0.04	-0.11		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR GGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1508	1evs	D	911	1082	3.4e-23	0.20	0.00		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR GGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1508	1dgi	R	602	810	6e-22	-0.35	0.03		POLIOVIRUS RECEPTOR; CHAIN: R; VP1; CHAIN: 1; VP2; CHAIN: 2; VP3; CHAIN: 3; VP4; CHAIN: 4;	VIRUS/VIRAL PROTEIN, RECEPTOR CD155, PVR, HUMAN POLIOVIRUS, ELECTRON MICROSCOPY, 2 POLIOVIRUS-RECEPTOR COMPLEX, VIRUS/VIRAL PROTEIN, RECEPTOR CD155, PVR, HUMAN POLIOVIRUS,
1508	1dgi	R	641	889	1.3e-23	-0.09	0.16		POLIOVIRUS RECEPTOR; CHAIN: R; VP1; CHAIN: 1; VP2;	VIRUS/VIRAL PROTEIN, RECEPTOR CD155, PVR, HUMAN POLIOVIRUS,

SEQ NO:	PDB ID	CHAI ID	STAR T AA	END AA	Fsi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									CHAIN: 2; VP3; CHAIN: 3; VP4; CHAIN: 4;	ELECTRON MICROSCOPY, 2 POLIOVIRUS-RECEPTOR COMPLEX, VIRUS/VIRAL PROTEIN RECEPTOR
1508	1qgi	R	902	1184	3.4e-18	-0.35	0.00		POLIOVIRUS RECEPTOR; CHAIN: R; VP1; CHAIN: 1; VP2; CHAIN: 2; VP3; CHAIN: 3; VP4; CHAIN: 4;	VIRUS/VIRAL PROTEIN RECEPTOR CD155; PVR, HUMAN POLIOVIRUS, ELECTRON MICROSCOPY, 2 POLIOVIRUS-RECEPTOR COMPLEX, VIRUS/VIRAL PROTEIN RECEPTOR
1508	1epf	A	178	346	6.8e-17	0.02	0.30		NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	CELL ADHESION NCAM; NCAM, IMMUNOGLOBULIN FOLD, GLYCOPROTEIN
1508	1epf	A	266	433	5.1e-28	0.11	0.42		NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	CELL ADHESION NCAM; NCAM, IMMUNOGLOBULIN FOLD, GLYCOPROTEIN
1508	1epf	A	354	517	3.4e-17	0.09	0.22		NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	CELL ADHESION NCAM; NCAM, IMMUNOGLOBULIN FOLD, GLYCOPROTEIN
1508	1epf	A	452	645	3e-24	0.34	0.92		NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	CELL ADHESION NCAM; NCAM, IMMUNOGLOBULIN FOLD, GLYCOPROTEIN
1508	1epf	A	539	722	3.4e-25	0.23	0.07		NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	CELL ADHESION NCAM; NCAM, IMMUNOGLOBULIN FOLD, GLYCOPROTEIN
1508	1epf	A	644	798	1.7e-20	0.02	0.99		NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	CELL ADHESION NCAM; NCAM, IMMUNOGLOBULIN FOLD, GLYCOPROTEIN
1508	1epf	A	815	997	4.5e-22	0.16	0.01		NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	CELL ADHESION NCAM; NCAM, IMMUNOGLOBULIN FOLD, GLYCOPROTEIN
1508	1epf	A	818	982	6.8e-19	0.25	0.75		NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	CELL ADHESION NCAM; NCAM, IMMUNOGLOBULIN FOLD, GLYCOPROTEIN
1508	1ev2	E	271	447	1e-29	-0.16	0.24		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGFR2; FGFR2;

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1508	1ev2	E	361	535	5.1e-22	0.10	0.04		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1508	1ev2	E	454	628	1e-33	-0.05	0.07		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1508	1ev2	E	825	996	1.7e-31	0.06	-0.11		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1508	1ev2	G	1009	1188	5.1e-35	0.10	0.01		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1508	1ev2	G	178	350	8.5e-21	0.02	0.43		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1508	1ev2	G	1	152	8.5e-18	0.01	-0.05		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGF2; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1508	1ev2	G	271	451	1.2e-32	0.13	0.18		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGF2; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1508	1ev2	G	361	538	6.8e-24	0.41	0.69		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGF2; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1508	1ev2	G	454	628	6.8e-34	-0.02	0.06		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGF2; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1508	1ev2	G	549	724	1.7e-23	0.23	0.53		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGF2; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1508	1ev2	G	61	264	1.2e-21	0.12	0.17		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGF2; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1508	1ev2	G	651	816	6.8e-34	-0.35	0.15		E, F, G, H; FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG)-LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1508	1ev2	G	737	900	3.4e-25	0.08	0.23		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG)-LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1508	1ev2	G	74	259	1.5e-22	0.18	0.51		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG)-LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1508	1ev2	G	825	1000	1.7e-33	0.04	-0.15		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG)-LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1508	1ev2	G	911	1087	6.8e-22	0.02	-0.01		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG)-LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1508	1ev1	C	178	346	5.1e-21	-0.26	0.33		FIBROBLAST GROWTH FACTOR 1; CHAIN: A, B;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF1; FGFR1;

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I- SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1508	1evt	C	271	447	8.5e-32	0.01	-0.06		FIBROBLAST GROWTH FACTOR 1; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF1; FGFRI; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I- SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1508	1evt	C	2	146	3.4e-19	0.23	-0.09		FIBROBLAST GROWTH FACTOR 1; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF1; FGFRI; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I- SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1508	1evt	C	450	628	3.4e-33	-0.15	0.18		FIBROBLAST GROWTH FACTOR 1; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF1; FGFRI; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I- SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1508	1evt	C	552	703	3e-16	-0.01	0.19		FIBROBLAST GROWTH FACTOR 1; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF1; FGFRI; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I- SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1508	1evt	C	61	260	1.2e-22	0.16	0.04		FIBROBLAST GROWTH FACTOR 1; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF1; FGFRI; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I- SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1508	1evt	C	642	812	1.4e-35	-0.32	0.11		FIBROBLAST GROWTH FACTOR 1; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGFI; FGRI; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE 1- SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS; B-TREFOIL FOLD
1508	1evt	C	737	896	1.2e-24	0.05	-0.03		FIBROBLAST GROWTH FACTOR 1; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGFI; FGRI; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE 1- SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS; B-TREFOIL FOLD
1508	1l2q	A	349	558	1.5e-17	0.14	0.06		HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A;	IMMUNE SYSTEM FC-EPSILON RI-ALPHA; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN
1508	1l2q	A	39	153	3e-21	0.32	0.48		HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A;	IMMUNE SYSTEM FC-EPSILON RI-ALPHA; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN
1508	1l2q	A	415	559	1.5e-20	0.26	0.92		HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A;	IMMUNE SYSTEM FC-EPSILON RI-ALPHA; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN
1508	1l2q	A	605	727	9e-18	-0.01	0.63		HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A;	IMMUNE SYSTEM FC-EPSILON RI-ALPHA; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN
1508	1l2q	A	646	795	1.7e-21	0.05	0.17		HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A;	IMMUNE SYSTEM FC-EPSILON RI-ALPHA; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN
1508	1l2q	A	779	900	3e-19	0.04	0.12		HIGH AFFINITY IMMUNOGLOBULIN EPSILON	IMMUNE SYSTEM FC-EPSILON RI-ALPHA; IMMUNOGLOBULIN FOLD,

SEQ NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1508	1f6a	A	258	430	3.4e-19	-0.01	0.01		RECEPTOR CHAIN: A; HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A; IG EPSILON CHAIN C REGION; CHAIN: B, D;	GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN IMMUNE SYSTEM HIGH AFFINITY IGE-FC RECEPTOR, FC(EPSILON) IGE-FC; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN, IGE ANTIBODY, IGE-FC
1508	1f6a	A	346	538	3.4e-17	0.09	-0.02		HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A; IG EPSILON CHAIN C REGION; CHAIN: B, D;	IMMUNE SYSTEM HIGH AFFINITY IGE-FC RECEPTOR, FC(EPSILON) IGE-FC; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN, IGE ANTIBODY, IGE-FC
1508	1f6a	A	39	152	6e-21	0.16	0.30		HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A; IG EPSILON CHAIN C REGION; CHAIN: B, D;	IMMUNE SYSTEM HIGH AFFINITY IGE-FC RECEPTOR, FC(EPSILON) IGE-FC; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN, IGE ANTIBODY, IGE-FC
1508	1f6a	A	415	538	9e-20	0.35	0.24		HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A; IG EPSILON CHAIN C REGION; CHAIN: B, D;	IMMUNE SYSTEM HIGH AFFINITY IGE-FC RECEPTOR, FC(EPSILON) IGE-FC; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN, IGE ANTIBODY, IGE-FC
1508	1f6a	A	451	645	7.5e-19	0.21	0.70		HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A; IG EPSILON CHAIN C REGION; CHAIN: B, D;	IMMUNE SYSTEM HIGH AFFINITY IGE-FC RECEPTOR, FC(EPSILON) IGE-FC; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN, IGE ANTIBODY, IGE-FC
1508	1f6a	A	566	726	7.5e-19	0.37	0.95		HIGH AFFINITY IMMUNOGLOBULIN EPSILON	IMMUNE SYSTEM HIGH AFFINITY IGE-FC RECEPTOR, FC(EPSILON)

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Coumpound	PDB annotation
									RECEPTOR CHAIN: A; IG EPSILON CHAIN C REGION; CHAIN: B, D;	IGE-FC; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN, IGE ANTIBODY, IGE-FC
1508	1fga	A	5	152	1e-16	0.20	-0.11		HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A; IG EPSILON CHAIN C REGION; CHAIN: B, D;	IMMUNE SYSTEM: HIGH AFFINITY IGE-FC RECEPTOR, FC(EPSILON) IGE-FC; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN, IGE ANTIBODY, IGE-FC
1508	1fga	A	646	795	1.4e-20	-0.14	0.11		HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A; IG EPSILON CHAIN C REGION; CHAIN: B, D;	IMMUNE SYSTEM: HIGH AFFINITY IGE-FC RECEPTOR, FC(EPSILON) IGE-FC; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN, IGE ANTIBODY, IGE-FC
1508	1fga	A	740	900	1.5e-19	0.27	0.10		HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A; IG EPSILON CHAIN C REGION; CHAIN: B, D;	IMMUNE SYSTEM: HIGH AFFINITY IGE-FC RECEPTOR, FC(EPSILON) IGE-FC; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN, IGE ANTIBODY, IGE-FC
1508	1fga	A	821	999	1.5e-15	0.11	0.63		HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A; IG EPSILON CHAIN C REGION; CHAIN: B, D;	IMMUNE SYSTEM: HIGH AFFINITY IGE-FC RECEPTOR, FC(EPSILON) IGE-FC; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN, IGE ANTIBODY, IGE-FC
1508	1fgg	A	349	534	1.2e-17	0.38	0.55		FC RECEPTOR FCGAMMAJRIIA; CHAIN: A;	IMMUNE SYSTEM: MEMBRANE PROTEIN CD32; FC RECEPTOR, IMMUNOGLOBULIN, LEUKOCYTE, CD32
1508	1fgg	A	37	148	3e-19	0.28	0.86		FC RECEPTOR FCGAMMAJRIIA; CHAIN: A;	IMMUNE SYSTEM, MEMBRANE PROTEIN CD32; FC RECEPTOR,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1508	1fsg	A	456	645	6e-19	0.02	0.43		FC RECEPTOR FC(GAMMA)RIIA; CHAIN: A;	IMMUNOGLOBULIN, LEUKOCYTE, CD32
1508	1fcg	A	820	997	6.8e-17	-0.26	0.53		FC RECEPTOR FC(GAMMA)RIIA; CHAIN: A;	IMMUNE SYSTEM, MEMBRANE PROTEIN CD32; FC RECEPTOR, IMMUNOGLOBULIN, LEUKOCYTE, CD32
1508	1fhg	A	1085	1186	8.5e-16	0.20	0.03		TELOKIN; CHAIN: A	IMMUNE SYSTEM, MEMBRANE PROTEIN CD32; FC RECEPTOR, IMMUNOGLOBULIN, LEUKOCYTE, CD32
1508	1fhg	A	347	447	8.5e-17	-0.28	0.00		TELOKIN; CHAIN: A	CONTRACTILE PROTEIN IMMUNOGLOBULIN FOLD, BETA BARREL
1508	1fhl	A	36	148	3e-18	0.29	0.54		LOW AFFINITY IMMUNOGLOBULIN GAMMA FC REGION CHAIN: A;	CONTRACTILE PROTEIN IMMUNOGLOBULIN FOLD, BETA BARREL
1508	1fhl	A	646	796	3.4e-16	0.03	0.41		LOW AFFINITY IMMUNOGLOBULIN GAMMA FC REGION CHAIN: A;	IMMUNE SYSTEM RECEPTOR BETA SANDWICH, IMMUNOGLOBULIN-LIKE, RECEPTOR
1508	1ge1	L	352	518	1.7e-15	0.17	0.60		ENVELOPE PROTEIN GP120; CHAIN: G; CD4; CHAIN: C; ANTIBODY 17B; CHAIN: L, H;	IMMUNE SYSTEM RECEPTOR BETA SANDWICH, IMMUNOGLOBULIN-LIKE, RECEPTOR COMPLEX (HIV ENVELOPE PROTEIN/CD4/FAB) COMPLEX (HIV ENVELOPE PROTEIN/CD4/FAB), HIV-1 EXTERIOR 2 ENVELOPE GP120, T-CELL SURFACE GLYCOPROTEIN CD4, 3 ANTIGEN-BINDING FRAGMENT OF HUMAN IMMUNOGLOBULIN 17B, 4 GLYCOSYLATED PROTEIN
1508	1lhg	A	557	703	6e-19	-0.34	0.06		T LYMPHOCYTE ADHESION GLYCOPROTEIN CD2 (RA17) IHNG 3	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1508	1hng	A	825	996	9e-15	0.06	0.17		T LYMPHOCYTE ADHESION GLYCOPROTEIN CD2 (RAT) 1HNG.3	
1508	1lhb	B	462	679	1.5e-20	-0.02	0.18		INTERLEUKIN-1 BETA; CHAIN: A; TYPE 1 INTERLEUKIN-1 RECEPTOR; CHAIN: B;	COMPLEX (IMMUNOGLOBULIN/RECEPTOR) IMMUNOGLOBULIN FOLD, TRANSMEMBRANE, GLYCOPROTEIN, RECEPTOR, 2 SIGNAL, COMPLEX (IMMUNOGLOBULIN/RECEPTOR)
1508	1lhb	B	740	996	3e-20	0.42	0.09		INTERLEUKIN-1 BETA; CHAIN: A; TYPE 1 INTERLEUKIN-1 RECEPTOR; CHAIN: B;	COMPLEX (IMMUNOGLOBULIN/RECEPTOR) IMMUNOGLOBULIN FOLD, TRANSMEMBRANE, GLYCOPROTEIN, RECEPTOR, 2 SIGNAL, COMPLEX (IMMUNOGLOBULIN/RECEPTOR)
1508	1lhb	B	747	994	1.7e-15	0.10	0.55		INTERLEUKIN-1 BETA; CHAIN: A; TYPE 1 INTERLEUKIN-1 RECEPTOR; CHAIN: B;	COMPLEX (IMMUNOGLOBULIN/RECEPTOR) IMMUNOGLOBULIN FOLD, TRANSMEMBRANE, GLYCOPROTEIN, RECEPTOR, 2 SIGNAL, COMPLEX (IMMUNOGLOBULIN/RECEPTOR)
1508	1lca		1084	1185	3.4e-14	0.14	0.59		TWITCHIN; CHAIN: NULL;	KINASE KINASE, TWITCHIN, INTRASTERIC REGULATION
1508	1lil	A	355	531	8.5e-16	0.20	0.60		LAMBDA III BENCE JONES PROTEIN CLE; CHAIN: A, B	IMMUNOGLOBULIN IMMUNOGLOBULIN, BENCE JONES PROTEIN
1508	1mco	H	143	543	5.1e-17			104.67	IMMUNOGLOBULIN IMMUNOGLOBULIN G1 (GG1) (MCO) WITH A HINGE DELETION IMCO.3	
1508	1mco	H	538	884	1.5e-17	-0.05	0.23		IMMUNOGLOBULIN	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									IMMUNOGLOBULIN G1 (JGG1) (MCG) WITH A HINGE DELETION IMCO.3	
1508	Inet		1086	1185	1.7e-14	0.58	0.53		TITIN; CHAIN: NULL;	MUSCLE PROTEIN CONNECTIN, NEXTM5; CELL ADHESION, GLYCOPROTEIN, TRANSMEMBRANE, REPEAT, BRAIN, 2 IMMUNOGLOBULIN FOLD, ALTERNATIVE SPLICING, SIGNAL, 3 MUSCLE PROTEIN
1508	Inet		178	262	3.4e-11	-0.53	0.00		TITIN; CHAIN: NULL;	MUSCLE PROTEIN CONNECTIN, NEXTM5; CELL ADHESION, GLYCOPROTEIN, TRANSMEMBRANE, REPEAT, BRAIN, 2 IMMUNOGLOBULIN FOLD, ALTERNATIVE SPLICING, SIGNAL, 3 MUSCLE PROTEIN
1508	Inet		349	449	5.1e-15	0.16	-0.12		TITIN; CHAIN: NULL;	MUSCLE PROTEIN CONNECTIN, NEXTM5; CELL ADHESION, GLYCOPROTEIN, TRANSMEMBRANE, REPEAT, BRAIN, 2 IMMUNOGLOBULIN FOLD, ALTERNATIVE SPLICING, SIGNAL, 3 MUSCLE PROTEIN
1508	Inet		643	721	1.7e-13	0.46	0.04		TITIN; CHAIN: NULL;	MUSCLE PROTEIN CONNECTIN, NEXTM5; CELL ADHESION, GLYCOPROTEIN, TRANSMEMBRANE, REPEAT, BRAIN, 2 IMMUNOGLOBULIN FOLD, ALTERNATIVE SPLICING, SIGNAL, 3 MUSCLE PROTEIN
1508	Inet		26	149	3.4e-10	0.11	-0.07		P58-CL42 KIR; CHAIN: NULL;	MUSCLE PROTEIN INHIBITORY RECEPTOR KILLER CELL INHIBITORY RECEPTOR, INHIBITORY RECEPTOR, NATURAL

SEQ ID NO:	PDB ID	CHAIN ID	STAR T.AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1508	1akr		813	995	1.7e-23	-0.01	0.13		P58-CL42 KIR; CHAIN: NULL;	KILLER CELLS, IMMUNOLOGICAL 2 RECEPTORS, IMMUNOGLOBULIN FOLD
1508	1tm		1088	1185	1.7e-14	0.63	0.35		MUSCLE PROTEIN TITIN MODULE M5 (CONNECTIN) 1TNM 3 (NMR, MINIMIZED AVERAGE STRUCTURE) 1TNM 4 1TNM 58	INHIBITORY RECEPTOR KILLER CELL INHIBITORY RECEPTOR; INHIBITORY RECEPTOR, NATURAL KILLER CELLS, IMMUNOLOGICAL 2 RECEPTORS, IMMUNOGLOBULIN FOLD
1508	1tm		178	262	3.4e-11	-0.22	0.00		MUSCLE PROTEIN TITIN MODULE M5 (CONNECTIN) 1TNM 3 (NMR, MINIMIZED AVERAGE STRUCTURE) 1TNM 4 1TNM 58	
1508	1tm		2	61	1.5e-09	0.30	-0.15		MUSCLE PROTEIN TITIN MODULE M5 (CONNECTIN) 1TNM 3 (NMR, MINIMIZED AVERAGE STRUCTURE) 1TNM 4 1TNM 58	
1508	1tm		643	721	1.7e-13	0.50	0.04		MUSCLE PROTEIN TITIN MODULE M5 (CONNECTIN) 1TNM 3 (NMR, MINIMIZED AVERAGE STRUCTURE) 1TNM 4 1TNM 58	
1508	1vea	A	397	538	4.5e-15	-0.05	0.72		HUMAN VASCULAR CELL ADHESION MOLECULE-1; 1VCA 4 CHAIN: A, B; 1VCA 5	CELL ADHESION PROTEIN VCAM-D1.2; 1VCA 6 IMMUNOGLOBULIN SUPERFAMILY, INTEGRIN-BINDING 1VCA 15
1508	1vea	A	557	680	4.5e-13	-0.15	0.00		HUMAN VASCULAR CELL	CELL ADHESION PROTEIN VCAM-

SEQ ID NO:	PDB ID	CHAIN	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									ADHESION MOLECULE-1; IVCA 4 CHAIN: A, B; IVCA 5	DL2: IVCA 6 IMMUNOGLOBULIN SUPERFAMILY, INTEGRIN-BINDING IVCA 15
1508	1wio	A	364	703	1.2e-26	0.09	0.41		T-CELL SURFACE GLYCOPROTEIN CD4; CHAIN: A, B;	GLYCOPROTEIN CD4; IMMUNOGLOBULIN FOLD, TRANSMEMBRANE, GLYCOPROTEIN, T-CELL, 2 MHC LIPOPROTEIN, POLYMORPHISM
1508	1wio	A	552	882	6e-26	-0.11	0.13		T-CELL SURFACE GLYCOPROTEIN CD4; CHAIN: A, B;	GLYCOPROTEIN CD4; IMMUNOGLOBULIN FOLD, TRANSMEMBRANE, GLYCOPROTEIN, T-CELL, 2 MHC LIPOPROTEIN, POLYMORPHISM
1508	1wio	A	740	1068	6e-23	0.06	0.68		T-CELL SURFACE GLYCOPROTEIN CD4; CHAIN: A, B;	GLYCOPROTEIN CD4; IMMUNOGLOBULIN FOLD, TRANSMEMBRANE, GLYCOPROTEIN, T-CELL, 2 MHC LIPOPROTEIN, POLYMORPHISM
1508	1zqx		821	1000	1.5e-16	-0.09	0.05		INTERCELLULAR ADHESION MOLECULE-2; CHAIN: NULL;	CELL ADHESION ICAM-2; IMMUNOGLOBULIN FOLD, CELL ADHESION, GLYCOPROTEIN, 2 TRANSMEMBRANE, REPEAT, SIGNAL
1508	2dli	A	347	534	1.2e-19	0.19	-0.09		MHC CLASS I NK CELL RECEPTOR PRECURSOR; CHAIN: A;	IMMUNE SYSTEM P58 NATURAL KILLER CELL RECEPTOR; KIR, NATURAL KILLER RECEPTOR, INHIBITORY RECEPTOR, 2
1508	2dli	A	451	643	4.5e-24	0.28	0.05		MHC CLASS I NK CELL RECEPTOR PRECURSOR; CHAIN: A;	IMMUNE SYSTEM P58 NATURAL KILLER CELL RECEPTOR; KIR, NATURAL KILLER RECEPTOR, INHIBITORY RECEPTOR, 2
1508	2dli	A	536	723	3e-16	0.00	0.19		MHC CLASS I NK CELL	IMMUNOGLOBULIN IMMUNE SYSTEM P58 NATURAL

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									RECEPTOR PRECURSOR; CHAIN: A;	KILLER CELL RECEPTOR, KIR, NATURAL KILLER RECEPTOR, INHIBITORY RECEPTOR, 2 IMMUNOGLOBULIN
1508	2dli	A	67	256	3e-21	0.20	0.23		MHC CLASS I NK CELL RECEPTOR PRECURSOR; CHAIN: A;	IMMUNE SYSTEM P8 NATURAL KILLER CELL RECEPTOR, KIR, NATURAL KILLER RECEPTOR, INHIBITORY RECEPTOR, 2 IMMUNOGLOBULIN
1508	2dli	A	7	148	1.2e-09	0.22	-0.06		MHC CLASS I NK CELL RECEPTOR PRECURSOR; CHAIN: A;	IMMUNE SYSTEM P8 NATURAL KILLER CELL RECEPTOR, KIR, NATURAL KILLER RECEPTOR, INHIBITORY RECEPTOR, 2 IMMUNOGLOBULIN
1508	2dli	A	813	991	5.1e-22	0.17	-0.06		MHC CLASS I NK CELL RECEPTOR PRECURSOR; CHAIN: A;	IMMUNE SYSTEM P8 NATURAL KILLER CELL RECEPTOR, KIR, NATURAL KILLER RECEPTOR, INHIBITORY RECEPTOR, 2 IMMUNOGLOBULIN
1508	2fcb	A	152	349	7.5e-15	0.01	-0.02		FC GAMMA RIIB; CHAIN: A;	IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32; IMMUNE SYSTEM
1508	2fcb	A	349	537	3.4e-18	0.25	0.27		FC GAMMA RIIB; CHAIN: A;	IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32; IMMUNE SYSTEM
1508	2fcb	A	37	151	7.5e-21	0.28	0.75		FC GAMMA RIIB; CHAIN: A;	IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32; IMMUNE SYSTEM
1508	2fcb	A	415	536	3e-20	-0.04	0.65		FC GAMMA RIIB; CHAIN: A;	IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32; IMMUNE SYSTEM
1508	2fcb	A	528	724	1.2e-16	0.19	0.65		FC GAMMA RIIB; CHAIN: A;	IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32; IMMUNE SYSTEM
1508	2fcb	A	740	898	3e-20	0.38	0.47		FC GAMMA RIIB; CHAIN: A;	IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32; IMMUNE SYSTEM
1508	2fcb	A	820	999	3.4e-17	0.04	0.00		FC GAMMA RIIB; CHAIN: A;	IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32; IMMUNE SYSTEM
1508	2fcb	A	825	998	4.5e-19	0.08	-0.05		FC GAMMA RIIB; CHAIN: A;	IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32; IMMUNE SYSTEM

SEQ ID NO:	PDB ID	CHAI ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1508	26b	A	917	1086	3e-18	0.00	0.70		FC GAMMA RIIB; CHAIN: A;	FC, CD32, IMMUNE SYSTEM IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32, IMMUNE SYSTEM
1508	3ncm	A	642	722	1.7e-12	0.42	0.12		NEURAL CELL ADHESION MOLECULE, LARGE ISOFORM; CHAIN: A;	CELL ADHESION PROTEIN NCAM MODULE 2; CELL ADHESION, GLYCOPROTEIN, HEPARIN-BINDING, GPI-ANCHOR, 2 NEURAL ADHESION MOLECULE, IMMUNOGLOBULIN FOLD, HOMOPHILIC 3 BINDING, CELL ADHESION PROTEIN
1508	8fab	A	353	529	5.1e-18	0.05	0.47		IMMUNOGLOBULIN FAB FRAGMENT FROM HUMAN IMMUNOGLOBULIN IGG1 (LAMBDA, HIL) 8FAB 3	
1510	1c7j	A	4	64	9e-13	-0.24	0.22		PARA-NITROBENZYL ESTERASE; CHAIN: A;	HYDROLASE PNB ESTERASE; ALPHA-BETA HYDROLASE, DIRECTED EVOLUTION, ORGANIC ACTIVITY, 2 PNB ESTERASE
1510	1ea5	A	3	73	1e-21	-0.23	0.12		ACETYLCHOLINESTERASE; CHAIN: A;	CHOLINESTERASE SERINE HYDROLASE, NEUROTRANSMITTER CLEAVAGE, CATALYTIC 2 TRIAD, ALPHA/BETA HYDROLASE
1510	1maa	A	3	73	5.1e-22	-0.29	0.43		ACETYLCHOLINESTERASE; CHAIN: A, B, C, D;	HYDROLASE MACHE; HYDROLASE, SERINE ESTERASE, ACETYLCHOLINESTERASE, TETRAMER, 2 HYDROLASE FOLD, GLYCOSTYLATED PROTEIN
1510	2bce		3	74	3.4e-19	-0.50	0.06		CHOLESTEROL ESTERASE; CHAIN: NULL;	HYDROLASE BILE SALT ACTIVATED LIPASE, BILE SALT STIMULATED HYDROLASE, SERINE ESTERASE, LIPASE

SEQ NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1512	1mev	G	241	274	3.4e-08	0.14	-0.11		DNA; CHAIN: A, B, D, E; CONSENSUS: ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1512	2adr		1	39	5.1e-11	-0.78	0.03		ADRI; CHAIN: NULL;	TRANSCRIPTION REGULATION, TRANSCRIPTION REGULATION, ADRI, ZINC FINGER, NMR
1512	2adr		403	446	1.7e-11	0.09	-0.20		ADRI; CHAIN: NULL;	TRANSCRIPTION REGULATION, TRANSCRIPTION REGULATION, ADRI, ZINC FINGER, NMR
1514	2pro	A	81	166	4.5e-10	0.03	-0.19		ALPHA-LYTIC PROTEASE; CHAIN: A, B, C;	PRO REGION PRO REGION, FOLDASE, PROTEIN FOLDING, SERINE PROTEASE
1515	1e23	A	432	503	4.5e-09	-0.01	0.09		SYNTAXIN-1A; CHAIN: A, B, C;	ENDOCYTOSIS/EXOCYTOSIS, SYNAPTOTAGMIN ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELIX BUNDLE
1521	1a4y	A	164	500	5.1e-25	0.21	1.00		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2, MOLECULAR RECOGNITION, EPTOPE MAPPING, LEUCINE-RICH 3 REPEATS
1521	1a4y	A	243	469	3e-34	0.34	1.00		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2, MOLECULAR RECOGNITION, EPTOPE MAPPING, LEUCINE-RICH 3 REPEATS

SEQ NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1521	1a4y	A	282	469	3e-35	0.51	1.00		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPTOPE MAPPING, LEUCINE-RICH 3 REPEATS
1521	1a4y	A	2	407	3.4e-24	0.05	0.95		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPTOPE MAPPING, LEUCINE-RICH 3 REPEATS
1521	1a4y	A	2	496	6.8e-32			113.01	RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPTOPE MAPPING, LEUCINE-RICH 3 REPEATS
1521	1a4y	A	86	471	6.8e-32	-0.03	0.90		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPTOPE MAPPING, LEUCINE-RICH 3 REPEATS
1521	1a0b	A	267	438	1.2e-23	-0.27	0.48		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1521	1a0b	A	316	495	1.7e-21	-0.30	0.39		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1521	1aee	A	350	474	1.7e-10	0.07	0.19		RAB GERANYLGERANYLTRANSFERASE RASE ALPHA SUBUNIT; CHAIN: A, C; RAB	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N.

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									GERANYLGERANYLTRANSFERASE BETA SUBUNIT; CHAIN: B, D;	FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
1521	1lo1	A	401	471	1.5e-06	-0.04	0.39		NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP.RBD OR RRM) AND LEUCINE-RICH-REPEAT 2 (LRR)
1521	1lo1	B	401	471	1.5e-06	-0.07	0.28		NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP.RBD OR RRM) AND LEUCINE-RICH-REPEAT 2 (LRR)
1521	1f6w	A	254	512	1.7e-12	-0.00	0.03		SKP2; CHAIN: A, C, E, G, I, K, M, O; SKP1; CHAIN: B, D, F, H, J, L, N, P;	LIGASE CYCLIN A/CDK2-ASSOCIATED PROTEIN P45; CYCLIN A/CDK2-ASSOCIATED PROTEIN P19; SKP1, SKP2, F-BOX, LRR, LEUCINE-RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE
1521	1f52	A	323	514	8.5e-13	0.08	0.51		SKP2; CHAIN: A, C; SKP1; CHAIN: B, D;	LIGASE CYCLIN A/CDK2-ASSOCIATED P45; CYCLIN A/CDK2-ASSOCIATED P19; SKP1, SKP2, F-BOX, LRRS, LEUCINE-RICH REPEATS, SCF, 2 UBIQUITIN, E3, UBIQUITIN PROTEIN LIGASE
1521	1yrg	A	157	418	6.8e-19	-0.08	0.55		GTPASE-ACTIVATING PROTEIN RNA1_SCHPO; CHAIN: A, B;	TRANSCRIPTION RNA1P; RANGAP; GTPASE-ACTIVATING PROTEIN FOR SP1, GTPASE-ACTIVATING PROTEIN GAP, RNA1P, RANGAP, LRR, LEUCINE-2 RICH REPEAT PROTEIN, TWINNING, HEMIHEDRAL TWINNING, 3 MEROHEDRAL TWINNING, MEROHEDRY
1521	1yrg	A	215	474	5.1e-21	0.17	0.98		GTPASE-ACTIVATING PROTEIN RNA1_SCHPO;	TRANSCRIPTION RNA1P; RANGAP; GTPASE-ACTIVATING PROTEIN

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									CHAIN: A, B;	FOR SPI1, GTPASE-ACTIVATING PROTEIN, GAP, RNAIP, RANGAP, LRR, LEUCINE-2 RICH REPEAT PROTEIN, TWINNING, HEMIHEDRAL TWINNING, 3 MEROHEDRAL TWINNING,
1521	1yrg	A	243	469	4.5e-30	0.11	0.55		GTPASE-ACTIVATING PROTEIN RNA1_SCHPO; CHAIN: A, B;	TRANSCRIPTION RNAIP; RANGAP; GTPASE-ACTIVATING PROTEIN FOR SPI1, GTPASE-ACTIVATING PROTEIN, GAP, RNAIP, RANGAP, LRR, LEUCINE-2 RICH REPEAT PROTEIN, TWINNING, HEMIHEDRAL TWINNING, 3 MEROHEDRAL TWINNING,
1521	1yrg	A	348	508	3.4e-09	0.10	0.28		GTPASE-ACTIVATING PROTEIN RNA1_SCHPO; CHAIN: A, B;	TRANSCRIPTION RNAIP; RANGAP; GTPASE-ACTIVATING PROTEIN FOR SPI1, GTPASE-ACTIVATING PROTEIN, GAP, RNAIP, RANGAP, LRR, LEUCINE-2 RICH REPEAT PROTEIN, TWINNING, HEMIHEDRAL TWINNING, 3 MEROHEDRAL TWINNING,
1521	2bnh		42	491	8.5e-46			109.97	RIBONUCLEASE INHIBITOR; CHAIN: NULL;	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS
1521	2bnh		89	511	8.5e-46	0.12	0.81		RIBONUCLEASE INHIBITOR; CHAIN: NULL;	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS

SEQ NO:	PDB ID	CHAI ID	STAR TAA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1522	1c1g	A	54	142	4.3e-08	0.46	-0.20		TROPOMYOSIN; CHAIN: A, B, C, D	CONTRACTILE PROTEIN TROPOMYOSIN COILED-COIL ALPHA-HELICAL, CONTRACTILE PROTEIN
1522	1c1i		50	142	1.5e-08	0.36	-0.20		COLICIN IA; CHAIN: NULL;	TRANSMEMBRANE PROTEIN COLICIN, BACTERIOCIN, ION CHANNEL FORMATION
1522	1c23	A	50	143	1.1e-12	0.36	-0.14		SYNTAXIN-1A; CHAIN: A, B, C;	TRANSMEMBRANE 2 PROTEIN ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35 KDA PROTEIN, p35A, THREE HELIX BUNDLE
1522	1req	A	50	142	4.3e-08	0.11	-0.20		METHYLMALONYL-COA MUTASE; CHAIN: A, B, C, D;	ISOMERASE/ISOMERASE, MUTASE, INTRAMOLECULAR TRANSFERASE
1523	1f9v	B	17	82	1.7e-24	0.78	1.00		SKP2; CHAIN: A, C, E, G, I, K, M, O; SKP1; CHAIN: B, D, F, H, J, L, N, P;	LIGASE CYCLIN A/CDK2-ASSOCIATED PROTEIN P46; CYCLIN A/CDK2-ASSOCIATED PROTEIN P19; SKP1, SKP2, F-BOX, LRR, LEUCINE-RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE
1523	1fs1	B	17	82	1.7e-24	0.21	0.62		CYCLIN A/CDK2-ASSOCIATED P19; CHAIN: A, C; CYCLIN A/CDK2-ASSOCIATED P45; CHAIN: B, D;	LIGASE SKP2 F-BOX; SKP1, SKP2, F-BOX, LRR, LEUCINE-RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE
1523	1fs2	B	17	82	1.7e-24	0.48	0.99		SKP2; CHAIN: A, C; SKP1; CHAIN: B, D;	LIGASE CYCLIN A/CDK2-ASSOCIATED P45; CYCLIN A/CDK2-ASSOCIATED P19; SKP1, SKP2, F-BOX, LRRS, LEUCINE-RICH REPEATS, SCF, 2 UBIQUITIN, E3, UBIQUITIN PROTEIN LIGASE
1523	1vcb	B	17	80	3.4e-16	0.76	1.00		ELONGIN B; CHAIN: A, D, G, J; ELONGIN C; CHAIN: B, E, H, K; VHL; CHAIN: C, F, I, L;	TRANSCRIPTION TUMOR SUPPRESSOR, CANCER, UBIQUITIN, BETA SANDWICH, 2

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	FMF score	SEQFOL D score	Compound	PDB annotation
1523	1veb	B	17	84	3.4e-16			52.02	ELONGIN B; CHAIN: A, D, G, I; ELONGIN C; CHAIN: B, E, H, K; VHL; CHAIN: C, F, I, L;	TRANSCRIPTION, TRANSCRIPTIONAL ELONGATION TRANSCRIPTION, TUMOR SUPPRESSOR, CANCER, UBIQUITIN, BETA SANDWICH, 2 TRANSCRIPTION, TRANSCRIPTIONAL ELONGATION
1524	1pbw	A	122	291	6.8e-19	0.10	0.63		PHOSPHATIDYLINOSITOL 3-KINASE; CHAIN: A, B;	PHOSPHOTRANSFERASE RHOGAP DOMAIN; PHOSPHOTRANSFERASE, TPASE ACTIVATING PROTEIN, GAP, CDC42, 2 PHOSPHOINOSITIDE 3-KINASE, SH3 DOMAIN, SH2 DOMAIN, 3 SIGNAL TRANSDUCTION
1524	1pbw	A	125	304	4.5e-35	0.57	1.00		PHOSPHATIDYLINOSITOL 3-KINASE; CHAIN: A, B;	PHOSPHOTRANSFERASE RHOGAP DOMAIN; PHOSPHOTRANSFERASE, TPASE ACTIVATING PROTEIN, GAP, CDC42, 2 PHOSPHOINOSITIDE 3-KINASE, SH3 DOMAIN, SH2 DOMAIN, 3 SIGNAL TRANSDUCTION
1524	1pbw	B	107	312	3e-36			67.87	PHOSPHATIDYLINOSITOL 3-KINASE; CHAIN: A, B;	PHOSPHOTRANSFERASE RHOGAP DOMAIN; PHOSPHOTRANSFERASE, TPASE ACTIVATING PROTEIN, GAP, CDC42, 2 PHOSPHOINOSITIDE 3-KINASE, SH3 DOMAIN, SH2 DOMAIN, 3 SIGNAL TRANSDUCTION
1524	1pbw	B	122	291	6.8e-19	0.09	0.76		PHOSPHATIDYLINOSITOL 3-KINASE; CHAIN: A, B;	PHOSPHOTRANSFERASE RHOGAP DOMAIN; PHOSPHOTRANSFERASE, TPASE ACTIVATING PROTEIN, GAP, CDC42, 2 PHOSPHOINOSITIDE 3-KINASE, SH3 DOMAIN, SH2

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1524	1pbw	B	125	311	3e-36	0.44	0.95		PHOSPHATIDYLINOSITOL 3-KINASE; CHAIN: A, B;	DOMAIN, 3 SIGNAL TRANSDUCTION PHOSPHOTRANSFERASE RHOGAP DOMAIN; PHOSPHOTRANSFERASE, TPASE ACTIVATING PROTEIN, GAP; CDC42, 2 PHOSPHOINOSITIDE 3-KINASE, SH3 DOMAIN, SH2 DOMAIN, 3 SIGNAL TRANSDUCTION
1524	1rgp		112	308	1.5e-37	0.77	1.00		RHOGAP; CHAIN: NULL;	G-PROTEIN CDC42 GTPASE-ACTIVATING PROTEIN; G-PROTEIN, GAP, SIGNAL-TRANSDUCTION
1524	1rgp		88	277	1e-29	0.08	0.54		RHOGAP; CHAIN: NULL;	G-PROTEIN CDC42 GTPASE-ACTIVATING PROTEIN; G-PROTEIN, GAP, SIGNAL-TRANSDUCTION
1524	1rgp		88	308	1.5e-37			97.96	RHOGAP; CHAIN: NULL;	G-PROTEIN CDC42 GTPASE-ACTIVATING PROTEIN; G-PROTEIN, GAP, SIGNAL-TRANSDUCTION
1524	1tx4	A	112	308	7.5e-39	0.88	1.00		P50-RHOGAP; CHAIN: A; TRANSFORMING PROTEIN RHOA; CHAIN: B;	COMPLEX(GTPASE ACTIVATN/PROTO-ONCOGENE) GTPASE-ACTIVATING PROTEIN RHOGAP; COMPLEX (GTPASE ACTIVATION/PROTO-ONCOGENE), GTPASE, 2 TRANSITION STATE, GAP
1524	1tx4	A	91	304	1.7e-29	0.18	1.00		P50-RHOGAP; CHAIN: A; TRANSFORMING PROTEIN RHOA; CHAIN: B;	COMPLEX(GTPASE ACTIVATN/PROTO-ONCOGENE) GTPASE-ACTIVATING PROTEIN RHOGAP; COMPLEX (GTPASE ACTIVATION/PROTO-ONCOGENE), GTPASE, 2 TRANSITION STATE, GAP
1524	1tx4	A	91	308	7.5e-39			107.06	P50-RHOGAP; CHAIN: A; TRANSFORMING PROTEIN RHOA; CHAIN: B;	COMPLEX(GTPASE ACTIVATN/PROTO-ONCOGENE) GTPASE-ACTIVATING PROTEIN RHOGAP; COMPLEX (GTPASE

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										ACTIVATION/PROTO-ONCOGENE), GTPASE, 2 TRANSITION STATE, GAP
1525	1ayz	A	1	134	1e-40			92.22	UBIQUITIN-CONJUGATING ENZYME RAD6; CHAIN: A, B, C;	UBIQUITIN CONJUGATION UBC2; UBIQUITIN CONJUGATING, UBIQUITIN-CONJUGATING ENZYME
1525	1ayz	A	4	128	1e-40	0.61	1.00		UBIQUITIN-CONJUGATING ENZYME RAD6; CHAIN: A, B, C;	UBIQUITIN CONJUGATION UBC2; UBIQUITIN CONJUGATING, UBIQUITIN-CONJUGATING ENZYME
1525	1o4z	D	5	129	8.5e-33	0.36	0.99		UBIQUITIN-PROTEIN LIGASE E3A; CHAIN: A, B, C; UBIQUITIN CONJUGATING ENZYME E2; CHAIN: D;	LIGASE E6AP; UBC7; BILOBAL STRUCTURE, ELONGATED SHAPE, E3 UBIQUITIN LIGASE, E2 2 UBIQUITIN CONJUGATING ENZYME
1525	1o4z	D	5	129	8.5e-33			80.53	UBIQUITIN-PROTEIN LIGASE E3A; CHAIN: A, B, C; UBIQUITIN CONJUGATING ENZYME E2; CHAIN: D;	LIGASE E6AP; UBC7; BILOBAL STRUCTURE, ELONGATED SHAPE, E3 UBIQUITIN LIGASE, E2 2 UBIQUITIN CONJUGATING ENZYME
1525	1qeq	A	1	130	3.4e-51	0.57	1.00		UBIQUITIN CONJUGATING ENZYME E2; CHAIN: A;	LIGASE UBIQUITIN, UBIQUITIN-CONJUGATING ENZYME, YEAST
1525	1qeq	A	4	131	3.4e-51			106.20	UBIQUITIN CONJUGATING ENZYME; CHAIN: A;	UBIQUITIN-CONJUGATING ENZYME, YEAST
1525	1u0a	A	1	130	3.4e-38	0.83	1.00		UBC9; CHAIN: NULL;	UBIQUITIN-CONJUGATING ENZYME UBIQUITIN-CONJUGATING ENZYME; UBIQUITIN-CONJUGATING ENZYME, UBIQUITIN-DIRECTED 2 PROTEOLYSIS, CELL CYCLE CONTROL, LIGASE
1525	1u0a	A	1	131	3.4e-38			73.11	UBC9; CHAIN: NULL;	UBIQUITIN-CONJUGATING ENZYME UBIQUITIN-CONJUGATING ENZYME; UBIQUITIN-CONJUGATING

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	FMF score	SEQFOL D score	Compound	PDB annotation
										ENZYME, UBIQUITIN-DIRECTED 2 PROTEOLYSIS, CELL CYCLE CONTROL, LIGASE
1525	2auk		1	126	1.2e-41			96.00	UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	UBIQUITIN CONJUGATION UBC1; UBIQUITIN CONJUGATION, LIGASE
1525	2auk		1	127	1.2e-41	0.49	1.00		UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	UBIQUITIN CONJUGATION UBC1; UBIQUITIN CONJUGATION, LIGASE
1525	2a2c		1	132	1.5e-37			82.57	UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	UBIQUITIN CONJUGATION UBIQUITIN CARRIER PROTEIN, THIOESTER 2 BOND, LIGASE
1525	2a2c		3	124	1.5e-37	0.66	1.00		UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	UBIQUITIN CONJUGATION UBIQUITIN CARRIER PROTEIN, THIOESTER 2 BOND, LIGASE
1525	2a2z		2	132	1.7e-36			77.96	UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	UBIQUITIN CONJUGATION UBC7; UBIQUITIN CONJUGATION, LIGASE, YEAST
1525	2a2z		3	128	1.7e-36	0.80	1.00		UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	UBIQUITIN CONJUGATION UBC7; UBIQUITIN CONJUGATION, LIGASE, YEAST
1527	1a4y	A	10	338	5.1e-19	-0.14	0.03		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPIPTOP MAPPING, LEUCINE-RICH 3 REPEATS
1527	1a4y	A	10	473	3.4e-18			67.17	RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPIPTOP MAPPING, LEUCINE-RICH 3 REPEATS

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1527	1a4y	A	134	335	9e-28	0.07	0.68		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION EPTOPE MAPPING, LEUCINE-RICH 3 REPEATS
1527	1a4y	A	25	415	3.4e-18	0.27	0.76		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPTOPE MAPPING, LEUCINE-RICH 3 REPEATS
1527	1a4y	A	66	309	1.5e-34	0.36	0.99		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPTOPE MAPPING, LEUCINE-RICH 3 REPEATS
1527	1a6n	A	140	284	3e-25	0.50	0.60		U2 RNA HAIRPIN IV; CHAIN: Q; R; U2 A'; CHAIN: A, C; U2 B'; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP RIBONUCLEOPROTEIN
1527	1a6n	A	164	291	7.5e-24	0.25	0.01		U2 RNA HAIRPIN IV; CHAIN: Q; R; U2 A'; CHAIN: A, C; U2 B'; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP RIBONUCLEOPROTEIN
1527	1a6n	A	212	326	1.5e-14	0.36	0.22		U2 RNA HAIRPIN IV; CHAIN: Q; R; U2 A'; CHAIN: A, C; U2 B'; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP RIBONUCLEOPROTEIN
1527	1a6n	A	232	339	3.4e-07	0.18	0.13		U2 RNA HAIRPIN IV; CHAIN: Q; R; U2 A'; CHAIN: A, C; U2 B'; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP RIBONUCLEOPROTEIN

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Bias	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1527	1a9n	A	43	146	1.7e-07	0.42	0.68		U2 RNA HAIRPIN IV; CHAIN: Q; R; U2 A'; CHAIN: A, C; U2 B'; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1527	1a9n	A	51	187	1.5e-24	0.15	0.98		U2 RNA HAIRPIN IV; CHAIN: Q; R; U2 A'; CHAIN: A, C; U2 B'; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1527	1a9n	A	92	234	3e-26	0.23	0.43		U2 RNA HAIRPIN IV; CHAIN: Q; R; U2 A'; CHAIN: A, C; U2 B'; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1527	1a9n	C	140	290	4.5e-26	0.25	0.45		U2 RNA HAIRPIN IV; CHAIN: Q; R; U2 A'; CHAIN: A, C; U2 B'; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1527	1a9n	C	212	326	9e-15	0.37	0.27		U2 RNA HAIRPIN IV; CHAIN: Q; R; U2 A'; CHAIN: A, C; U2 B'; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1527	1a9n	C	23	95	3.4e-05	0.03	0.00		U2 RNA HAIRPIN IV; CHAIN: Q; R; U2 A'; CHAIN: A, C; U2 B'; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1527	1a9n	C	43	146	1.7e-07	0.36	0.43		U2 RNA HAIRPIN IV; CHAIN: Q; R; U2 A'; CHAIN: A, C; U2 B'; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1527	1a9n	C	51	187	3e-24	0.37	0.96		U2 RNA HAIRPIN IV; CHAIN: Q; R; U2 A'; CHAIN: A, C; U2 B'; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1527	1a9n	C	68	215	1e-24	0.16	0.70		U2 RNA HAIRPIN IV; CHAIN: Q; R; U2 A'; CHAIN: A, C; U2 B'; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1527	1a9n	C	92	234	3c-26	0.43	0.69		CHAIN: B, D; U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A; CHAIN: A, C, U2 B"; CHAIN: B, D;	(NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1527	1d0b	A	129	311	8.5e-24	0.35	0.99		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1527	1d0b	A	228	377	3.4e-18	-0.07	0.10		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1527	1d0b	A	4	188	3.4e-23	0.12	0.70		INTERNALIN R; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1527	1d0c	A	21	121	1.2e-10	0.31	0.15		RAB GERANYLGERANYLTRANSFERASE ALPHA SUBUNIT; CHAIN: A, C, RAB GERANYLGERANYLTRANSFERASE BETA SUBUNIT; CHAIN: B, D;	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N-FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
1527	1d59	A	167	291	1.5e-18	-0.40	0.06		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE-RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA
1527	1d59	A	217	338	5.1e-15	0.12	-0.09		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE-RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA
1527	1d59	A	43	145	1e-09	-0.08	0.23		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE-RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1527	1ds9	A	73	235	1.4e-11	-0.39	0.15		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE-RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CYLAMYDOMONAS, FLAGELLIN
1527	1f6l	A	227	308	3.4e-07	-0.15	0.01		NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP,RBD OR RRM) AND LEUCINE-RICH-REPEAT 2 (LRR)
1527	1f6l	B	227	308	3.4e-07	0.16	0.30		NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP,RBD OR RRM) AND LEUCINE-RICH-REPEAT 2 (LRR)
1527	1f6w	A	134	347	1.5e-15	-0.05	0.36		SKP2; CHAIN: A, C, E, G, I, K, M, O; SKP1; CHAIN: B, D, F, H, J, L, N, P;	LIGASE CYCLIN A/CDK2-ASSOCIATED PROTEIN P45; CYCLIN A/CDK2-ASSOCIATED PROTEIN P19; SKP1, SKP2, F-BOX, LRR, LEUCINE-RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE
1527	1f62	A	125	334	1.3e-20	0.21	-0.03		SKP2; CHAIN: A, C; SKP1; CHAIN: B, D;	LIGASE CYCLIN A/CDK2-ASSOCIATED P45; CYCLIN A/CDK2-ASSOCIATED P19; SKP1, SKP2, F-BOX, LRRS, LEUCINE-RICH REPEATS, SCF, 2 UBIQUITIN, E3, UBIQUITIN PROTEIN LIGASE
1527	1f62	A	171	311	5.1e-12	0.00	0.04		SKP2; CHAIN: A, C; SKP1; CHAIN: B, D;	LIGASE CYCLIN A/CDK2-ASSOCIATED P45; CYCLIN A/CDK2-ASSOCIATED P19; SKP1, SKP2, F-BOX, LRRS, LEUCINE-RICH REPEATS, SCF, 2 UBIQUITIN, E3, UBIQUITIN PROTEIN LIGASE
1527	1yrg	A	62	360	6.8e-12	0.16	-0.03		GTPASE-ACTIVATING PROTEIN RAN1; SCIPQ; CHAIN: A, B;	TRANSCRIPTION RNA1P; RANGAP; GTPASE-ACTIVATING PROTEIN FOR SPI1, GTPASE-ACTIVATING PROTEIN, GAP, RNA1P, RANGAP,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									POTASSIUM CHANNEL; CHAIN: A, B, C, D;	GATED POTASSIUM CHANNEL, TETRAMERIZATION DOMAIN, 2 INTRACELLULAR GATE, TETRAMER
1528	1tld	A	117	204	1.3e-11	0.26	0.45		POTASSIUM CHANNEL KVL1; CHAIN: A;	PROTON TRANSPORT POTASSIUM CHANNELS, TETRAMERIZATION DOMAIN, X-RAY STRUCTURE, 2 APLYSIA KVL1, PROTON TRANSPORT
1528	3kvt		117	217	6e-15	0.59	0.62		POTASSIUM CHANNEL PROTEIN SHAW; CHAIN: NULL;	POTASSIUM CHANNEL POTASSIUM CHANNEL, TETRAMERIZATION DOMAIN, MOLECULAR 2 RECOGNITION, ZINC-BINDING
1529	1a12	A	346	704	1.7e-49	0.04	-0.08		REGULATOR OF CHROMOSOME CONDENSATION I; CHAIN: A, B, C;	GUANINE NUCLEOTIDE EXCHANGE FACTOR RCC1; GUANINE NUCLEOTIDE EXCHANGE FACTOR, GEF, RAN, 2 RAS-LIKE NUCLEAR GTP BINDING PROTEIN HEADER
1529	1a12	A	354	741	1.7e-49			97.41	REGULATOR OF CHROMOSOME CONDENSATION I; CHAIN: A, B, C;	GUANINE NUCLEOTIDE EXCHANGE FACTOR RCC1; GUANINE NUCLEOTIDE EXCHANGE FACTOR, GEF, RAN, 2 RAS-LIKE NUCLEAR GTP BINDING PROTEIN HEADER
1529	1a12	A	9	415	6.8e-91	-0.01	0.22		REGULATOR OF CHROMOSOME CONDENSATION I; CHAIN: A, B, C;	GUANINE NUCLEOTIDE EXCHANGE FACTOR RCC1; GUANINE NUCLEOTIDE EXCHANGE FACTOR, GEF, RAN, 2 RAS-LIKE NUCLEAR GTP BINDING PROTEIN HEADER
1529	1dbt	A	695	1001	3e-16	-0.03	0.22		HUMAN SOS 1; CHAIN: A;	GENE REGULATION SON OF SEVENLESS PROTEIN; GUANINE

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1529	1fbo	A	930	1006	7.5e-07	-0.27	0.33		DUAL ADAPTOR OF PHOSPHOTYROSINE AND 3-CHAIN: A;	NUCLEOTIDE EXCHANGE FACTOR, GENE REGULATION SIGNALING PROTEIN DAPPI1, PHISH, BAM32; PLECKSTRIN, 3- PHOSPHOINOSITIDES, INOSITOL TETRAKISPHOSPHATE 2 SIGNAL TRANSDUCTION PROTEIN, ADAPTOR PROTEIN
1529	1fbs	A	930	1007	3e-07	0.02	0.35		DUAL ADAPTOR OF PHOSPHOTYROSINE AND 3-CHAIN: A;	SIGNALING PROTEIN DAPPI1, PHISH, BAM32; PLECKSTRIN, 3- PHOSPHOINOSITIDES, INOSITOL TETRAKISPHOSPHATE 2 SIGNAL TRANSDUCTION PROTEIN, ADAPTOR PROTEIN
1529	1pls		935	1007	0.0003	0.38	0.93		PHOSPHORYLATION PLECKSTRIN (N-TERMINAL PLECKSTRIN HOMOLOG DOMAIN) MUTANT 1PLS 3 WITH LEU GLU (HIS)6 ADDED TO THE C TERMINUS 1PLS 4 (INS(G105-LEHHHHH)) (NMR, 25 STRUCTURES) 1PLS 5	
1529	1pms		897	1004	1.5e-09	0.32	-0.02		SOS 1; CHAIN: NULL;	SIGNAL TRANSDUCTION SON OF SEVENLESS; PLECKSTRIN, SON OF SEVENLESS, SIGNAL TRANSDUCTION
1530	1dlj	A	2	138	6.8e-52	1.32	1.00		PROFILIN II; CHAIN: A, B, C, D;	CONTRACTILE PROTEIN ACIDIC PROFILIN ISOMER, ACTIN- BINDING PROTEIN, POLY-L-2 PROLINE BINDING PROTEIN, CONTRACTILE PROTEIN
1530	1dlj	A	2	138	9e-63	1.32	1.00		PROFILIN II; CHAIN: A, B, C, D;	CONTRACTILE PROTEIN ACIDIC PROFILIN ISOMER, ACTIN-

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										BINDING PROTEIN, POLY-L-2 PROLINE BINDING PROTEIN, CONTRACTILE PROTEIN
1530	1fl		2	140	1.7e-52	1.04	1.00		PROFILIN; CHAIN: NULL;	PROTEIN BINDING ACETYLATION, ACTIN-BINDING PROTEIN, MULTIGENE FAMILY
1530	1fl		2	140	1.7e-52			167.69	PROFILIN; CHAIN: NULL;	PROTEIN BINDING ACETYLATION, ACTIN-BINDING PROTEIN, MULTIGENE FAMILY
1530	1pue		2	140	1.7e-52	0.92	1.00		ACTIN BINDING PROTEIN	
1530	1pue		2	140	1.7e-52			167.40	PROFILIN IPNE 3	
									PROFILIN IPNE 3	
1531	1dij	A	2	122	1.7e-42	0.75	1.00		PROFILIN II; CHAIN: A, B, C, D;	CONTRACTILE PROTEIN ACIDIC PROFILIN ISOFORM, ACTIN-BINDING PROTEIN, POLY-L-2 PROLINE BINDING PROTEIN, CONTRACTILE PROTEIN
1531	1dij	A	2	122	4.5e-52	0.71	1.00		PROFILIN II; CHAIN: A, B, C, D;	CONTRACTILE PROTEIN ACIDIC PROFILIN ISOFORM, ACTIN-BINDING PROTEIN, POLY-L-2 PROLINE BINDING PROTEIN, CONTRACTILE PROTEIN
1531	1pue		2	124	1.5e-42	0.64	1.00		ACTIN BINDING PROTEIN	
1531	1pue		2	124	1.5e-42			133.14	PROFILIN IPNE 3	
1534	1log2		2	176	3e-68	-0.22	1.00		KINESIN; CHAIN: NULL;	MOTOR PROTEIN MOTOR PROTEIN, ATPASE, MICROTUBULE ASSOCIATED
1534	1log2		2	176	6.8e-35	-0.15	1.00		KINESIN; CHAIN: NULL;	MOTOR PROTEIN MOTOR PROTEIN, ATPASE, MICROTUBULE

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1534	1cz7	A	4	170	1e-17	-0.36	0.10		MICROTUBULE MOTOR PROTEIN NCD; CHAIN: A, B, C, D;	ASSOCIATED CONTRACTILE PROTEIN NCD, CLARET SEGREGATIONAL PROTEIN; NCD CRYSTAL STRUCTURE, MICROTUBULE MOTORS, KINESIN 2 SUPERFAMILY, CONTRACTILE PROTEIN
1534	2kin	B	101	186	3e-40	0.03	0.83		KINESIN; CHAIN: A, B;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
1534	2kin	B	101	199	6.8e-19	-0.17	1.00		KINESIN; CHAIN: A, B;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
1534	2ncd	A	4	170	6.8e-18	-0.24	0.54		KINESIN MOTOR NCD; CHAIN: A;	CONTRACTILE PROTEIN KINESIN, MICROTUBULE-BASED MOTOR, CYTOSKELETON
1534	3kar		1	172	1.7e-21	-0.30	0.66		KINESIN-LIKE PROTEIN KAR3; CHAIN: NULL;	CONTRACTILE PROTEIN NCD, CONTRACTILE PROTEIN
1534	3kin	B	105	186	1.5e-38	-0.25	0.98		KINESIN HEAVY CHAIN; CHAIN: A, B, C, D;	CONTRACTILE PROTEIN, KAR3, KINESIN-RELATED PROTEIN, MOTOR 2 PROTEIN, ATPASE, P-LOOP, MICROTUBULE BINDING PROTEIN
1534	3kin	B	105	230	1.7e-20	-0.44	0.71		KINESIN HEAVY CHAIN; CHAIN: A, B, C, D;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
1536	1ars		71	369	6.8e-13	-0.22	0.07		TRANSFERASE (AMINOTRANSFERASE) ASPARTATE AMINOTRANSFERASE (E.C.2.6.1.1) COMPLEXED WITH LARS 3 PYRIDOXAL-5'-PHOSPHATE LARS 4	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
1536	1bjw	A	1	369	5.1e-81	0.17	0.75		ASPARTATE AMINOTRANSFERASE; CHAIN: A, B;	AMINOTRANSFERASE AMINOTRANSFERASE, PYRIDOXAL ENZYME

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1536	1bs0	A	1	375	1.7e-41			69.72	8-AMINO-7-OXONANOATE SYNTHASE; CHAIN: A;	TRANSFERASE AONS, 8-AMINO-7-KETOPELARGONATE SYNTHASE; PLP-DEPENDENT ACYL-COA SYNTHASE, BIOTIN BIOSYNTHESIS, 8-2 AMINO-7-OXONANOATE SYNTHASE, 8-AMINO-7-KETOPELARGONATE 3 SYNTHASE, TRANSFERASE
1536	1bs0	A	47	365	1.7e-41	0.32	0.12		8-AMINO-7-OXONANOATE SYNTHASE; CHAIN: A;	TRANSFERASE AONS, 8-AMINO-7-KETOPELARGONATE SYNTHASE; PLP-DEPENDENT ACYL-COA SYNTHASE, BIOTIN BIOSYNTHESIS, 8-2 AMINO-7-OXONANOATE SYNTHASE, 8-AMINO-7-KETOPELARGONATE 3 SYNTHASE, TRANSFERASE
1536	1bw0	A	1	373	6.8e-54	0.09	0.16		TYROSINE AMINOTRANSFERASE; CHAIN: A, B;	TRANSFERASE TAT, TYROSINE CATABOLISM, TRANSFERASE, AMINOTRANSFERASE, 2
1536	1e7n	A	68	373	1.7e-18	-0.03	0.25		CRYSTALYSIN; CHAIN: A, B, C, D, E, F, G, H;	PYRIDOXAL-5-PHOSPHATE, PLP TRANSFERASE TRANSFERASE, AMINOTRANSFERASE, PYRIDOXAL PHOSPHATE
1536	1d2f	A	92	373	3.4e-21	0.10	-0.05		NALY PROTEIN; CHAIN: A, B;	TRANSFERASE AMINOTRANSFERASE FOLD, LARGE PLP-BINDING DOMAIN, SMALL C-2 TERMINAL DOMAIN, OPEN ALPHA BETA STRUCTURE
1536	1d7u	A	1	372	3.4e-63			169.86	2,2-DIALKYL GLYCINE DECARBOXYLASE (PYRUVATE); CHAIN: A;	LYASE DGD; ENZYME COMPLEXES, CATALYTIC MECHANISM, DECARBOXYLATION 2 INHIBITOR, LYASE
1536	1d7u	A	46	372	3.4e-63	0.72	1.00		2,2-DIALKYL GLYCINE DECARBOXYLASE	LYASE DGD; ENZYME COMPLEXES, CATALYTIC MECHANISM

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									(PYRUVATE); CHAIN: A;	DECARBOXYLATION 2 INHIBITOR, LYASE
1536	1gix	A	49	370	1.5e-70	0.71	1.00		4-AMINO BUTYRATE AMINOTRANSFERASE; CHAIN: A, B, C, D;	TRANSFERASE GABA-AT; PLP-DEPENDENT ENZYME, AMINOTRANSFERASE, 4-AMINO BUTYRIC ACID, 2 ANTI-EPILEPTIC DRUG TARGET
1536	1gix	A	53	373	1.7e-53	0.47	1.00		4-AMINO BUTYRATE AMINOTRANSFERASE; CHAIN: A, B, C, D;	TRANSFERASE GABA-AT; PLP-DEPENDENT ENZYME, AMINOTRANSFERASE, 4-AMINO BUTYRIC ACID, 2 ANTI-EPILEPTIC DRUG TARGET
1536	1qj5	A	40	371	6.8e-64	0.54	1.00		7,8-DIAMINOPELARGONIC ACID SYNTHASE; CHAIN: A, B;	AMINOTRANSFERASE AMINOTRANSFERASE, PYRIDOXAL-5'-PHOSPHATE, BIOTIN 2 BIOSYNTHESIS
1536	2gaa	A	1	372	1.2e-72			90.43	GLUTAMATE SEMIALDEHYDE AMINOTRANSFERASE; CHAIN: A, B;	CHLOROPHYLL BIOSYNTHESIS GLUTAMATE SEMIALDEHYDE AMINOTRANSFERASE, CHLOROPHYLL BIOSYNTHESIS, PYRIDOXAL-5'-PHOSPHATE, 2 PYRIDOXAMINE-5'-PHOSPHATE, ASYMMETRIC DIMER
1536	2gaa	A	5	372	1.2e-72	0.25	1.00		GLUTAMATE SEMIALDEHYDE AMINOTRANSFERASE; CHAIN: A, B;	CHLOROPHYLL BIOSYNTHESIS GLUTAMATE SEMIALDEHYDE AMINOTRANSFERASE, CHLOROPHYLL BIOSYNTHESIS, PYRIDOXAL-5'-PHOSPHATE, 2 PYRIDOXAMINE-5'-PHOSPHATE, ASYMMETRIC DIMER
1536	2oat	A	2	372	1.7e-62			130.71	ORNITHINE AMINOTRANSFERASE; CHAIN: A, B, C;	AMINOTRANSFERASE AMINOTRANSFERASE, 5-FLUOROMETHYLOORNITHINE, PLP-DEPENDENT 2 ENZYME, PYRIDOXAL PHOSPHATE
1536	2oat	A	40	369	1.7e-62	0.57	1.00		ORNITHINE	AMINOTRANSFERASE

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									AMINOTRANSFERASE; CHAIN: A, B, C;	AMINOTRANSFERASE, 5-FLUOROMETHYLTORNTHINE, PLP-DEPENDENT 2 ENZYME, PYRIDOXAL PHOSPHATE
1539	1cul	A	91	916	0	-0.16	0.04		CALCIUM-TRANSPORTING ATPASE SARCOPLASMIC CHAIN: A;	HYDROLASE SERCA1; ION PUMP, CALCIUM, MEMBRANE PROTEIN, P-TYPE ATPASE, ACTIVE 2 TRANSPORT
1541	1a17		135	247	3.4e-23	0.06	0.77		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	HYDROLASE TETRA/TRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE
1541	1a17		179	253	1e-10	-0.35	0.15		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	HYDROLASE TETRA/TRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE
1541	1e96	B	102	230	1.5e-13	-0.12	0.29		RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 1; CHAIN: A; NEUTROPHIL CYTOSOL FACTOR 2 (NCF-2) CHAIN: B;	SIGNALLING COMPLEX RAC1; P67H0X; SIGNALLING COMPLEX, GTPASE, NADPH OXIDASE, PROTEIN-PROTEIN 2 COMPLEX, TPR MOTIF
1541	1e1r	A	101	196	1e-12	0.21	0.54		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEVD; CHAIN: B;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
1541	1e1r	A	139	231	1e-18	0.00	0.19		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEVD; CHAIN: B;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
1541	1e1r	A	67	167	1e-18	0.26	0.52		TPR2A-DOMAIN OF HOP;	CHAPERONE HOP, TPR-DOMAIN,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
1541	1c1w	A	133	250	1.7e-20	-0.04	0.53		TPR1-DOMAIN OF HOP; CHAIN: A; B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
1541	1c1w	A	28	133	3.4e-15	0.50	0.01		TPR1-DOMAIN OF HOP; CHAIN: A; B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
1541	1c1w	A	64	175	1e-14	0.73	0.46		TPR1-DOMAIN OF HOP; CHAIN: A; B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
1541	1c1w	A	98	202	3.4e-13	0.35	0.37		TPR1-DOMAIN OF HOP; CHAIN: A; B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
1541	1c1h	A	6	252	8.5e-35	-0.06	0.18		PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A; B; PTS1-CONTAINING PEPTIDE; CHAIN: C, D;	SIGNALING PROTEIN PEROXISOMAL RECEPTOR 1, PTS1-BP, PEROXIN-5, PTS1 PROTEIN-PEPTIDE COMPLEX, TETRAPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT
1541	1cqe	A	2	254	3.4e-07			63.04	VESICULAR TRANSPORT PROTEIN SEC17; CHAIN: A;	PROTEIN TRANSPORT HELIX-TURN-HELIX TPR-LIKE REPEAT, PROTEIN TRANSPORT
1542	1c2h	A	65	190	3.4e-16	0.55	-0.09		GLYCINE-N-METHYLTRANSFERASE; CHAIN: A, B, C, D;	TRANSFERASE METHYLTRANSFERASE
1542	1dus	A	72	187	3.4e-09	0.57	0.37		M00882; CHAIN: A;	STRUCTURAL GENOMICS HYPOTHETICAL PROTEIN

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1542	1qun	A	72	200	3e-06	0.27	0.00		ERM ^c METHYLTRANSFERASE; CHAIN: A;	METHANOCOCUS JANNASCHII TRANSFERASE RNA METHYLTRANSFERASE ERM ^c , COPACTOR ANALOGS
1542	1kva	A	21	190	3.4e-17	-0.00	-0.13		GLYCINE N- METHYLTRANSFERASE; CHAIN: A, B;	METHYLTRANSFERASE GNMT, S- ADENOSYL-L-METHIONINE; GLYCINE METHYLTRANSFERASE
1542	2adm	A	66	192	5.1e-11	0.14	-0.14		ADENINE-NG-DNA- METHYLTRANSFERASE TAQI; CHAIN: A, B;	METHYLTRANSFERASE METHYLTRANSFERASE, RESTRICTION SYSTEM
1542	2adm	A	66	337	7.5e-06	-0.29	0.16		ADENINE-NG-DNA- METHYLTRANSFERASE TAQI; CHAIN: A, B;	METHYLTRANSFERASE TRANSFERASE METHYLTRANSFERASE, RESTRICTION SYSTEM
1544	1ai7		1	58	1.5e-06	-0.10	0.28		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	HYDROLASE TETRATRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE
1544	1fch	A	2	83	4.5e-06	0.17	0.25		PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTISI-CONTAINING PEPTIDE; CHAIN: C, D;	SIGNALING PROTEIN PEROXISOMAL RECEPTOR 1, PTISI- BP, PEROXIN-5, PTISI PROTEIN- PEPTIDE COMPLEX, TETRATRICOPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT
1545	1ald	P	228	291	5.1e-32			58.51	DNA-BINDING PROTEIN ANTENAPEDIA PROTEIN (HOMEOBOX) MUTANT WITH CYS 39 1AHD 3 REPLACED BY SER (C39S) COMPLEX WITH DNA (NMR),	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1545	1ahd	P	229	294	5.1e-32	0.01	1.00		1AHD 4 16 STRUCTURES) 1AHD 5	
									DNA-BINDING PROTEIN ANTENNAPEDIA PROTEIN (HOMEODOMAIN) MUTANT WITH CYS 39 1AHD 3 REPLACED BY SER (C39S) COMPLEX WITH DNA (NMR, 1AHD 4 16 STRUCTURES) 1AHD 5	
1545	1au7	A	212	286	4.5e-22	-0.40	0.59		PIT-1; CHAIN: A, B; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) GHE-1; COMPLEX (DNA-BINDING PROTEIN/DNA), PITUITARY, CPD, 2 POU DOMAIN, TRANSCRIPTION FACTOR
1545	1b72	A	224	290	3e-28			78.21	HOMEODOMAIN PROTEIN HOX-B1; CHAIN: A; PBX1; CHAIN: B; DNA CHAIN: D; DNA CHAIN: E;	PROTEIN/DNA HOMEODOMAIN, DNA, COMPLEX, DNA-BINDING PROTEIN, PROTEIN/DNA
1545	1b72	A	223	290	3e-28	0.40	1.00		HOMEODOMAIN PROTEIN HOX-B1; CHAIN: A; PBX1; CHAIN: B; DNA CHAIN: D; DNA CHAIN: E;	PROTEIN/DNA HOMEODOMAIN, DNA, COMPLEX, DNA-BINDING PROTEIN, PROTEIN/DNA
1545	1b72	A	223	290	5.1e-26	0.40	1.00		HOMEODOMAIN PROTEIN HOX-B1; CHAIN: A; PBX1; CHAIN: B; DNA CHAIN: D; DNA CHAIN: E;	PROTEIN/DNA HOMEODOMAIN, DNA, COMPLEX, DNA-BINDING PROTEIN, PROTEIN/DNA
1545	1b8l	A	226	287	5.1e-27			55.32	ULTRABITHORAX HOMEOTIC PROTEIN IV; CHAIN: A; HOMEODOMAIN PROTEIN EXTRADENTICLE; CHAIN: B; DNA (5' CHAIN: C; DNA (5' CHAIN: D;	TRANSCRIPTION/DNA ULTRABITHORAX; PBX PROTEIN; DNA BINDING, HOMEODOMAIN, HOMEOTIC PROTEINS, DEVELOPMENT, 2 SPECIFICITY
1545	1b8l	A	233	287	5.1e-27	0.49	1.00		ULTRABITHORAX HOMEOTIC PROTEIN IV; CHAIN: A; HOMEODOMAIN PROTEIN EXTRADENTICLE; CHAIN: B;	TRANSCRIPTION/DNA ULTRABITHORAX; PBX PROTEIN; DNA BINDING, HOMEODOMAIN, HOMEOTIC PROTEINS,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1545	1ftz		227	296	8.5e-28			59.53	DNA (5'- CHAIN: C; DNA (5'- CHAIN: D; DNA-BINDING FUSHI TARAZU PROTEIN (HOMEODOMAIN) (NMR, 20 STRUCTURES) 1FTZ 3	DEVELOPMENT, 2 SPECIFICITY
1545	1ftz		229	294	8.5e-28	-0.12	0.92		DNA-BINDING FUSHI TARAZU PROTEIN (HOMEODOMAIN) (NMR, 20 STRUCTURES) 1FTZ 3	
1545	1san		234	291	1.4e-29			57.26	DNA-BINDING PROTEIN ANTENNAPEDIA PROTEIN (HOMEODOMAIN) MUTANT WITH CYS 39 1SAN 3 REPLACED BY SER AND RESIDUES 1-6 DELETED (C39S,DEL 1-6) 1SAN 4 (NMR, 20 STRUCTURES) 1SAN 5	
1545	1san		235	294	1.4e-29	0.30	1.00		DNA-BINDING PROTEIN ANTENNAPEDIA PROTEIN (HOMEODOMAIN) MUTANT WITH CYS 39 1SAN 3 REPLACED BY SER AND RESIDUES 1-6 DELETED (C39S,DEL 1-6) 1SAN 4 (NMR, 20 STRUCTURES) 1SAN 5	
1545	9ant	A	233	288	1.7e-29	0.42	1.00		ANTENNAPEDIA PROTEIN; CHAIN: A, B; DNA; CHAIN: C, D, E, F;	COMPLEX (DNA-BINDING PROTEIN/DNA) HD; HOMEODOMAIN, COMPLEX (DNA-BINDING PROTEIN/DNA)
1545	9ant	A	233	288	1.7e-29			61.44	ANTENNAPEDIA PROTEIN; CHAIN: A, B; DNA; CHAIN: C, D, E, F;	COMPLEX (DNA-BINDING PROTEIN/DNA) HD; HOMEODOMAIN, COMPLEX (DNA-BINDING PROTEIN/DNA)
1546	1aih	A	12	92	1.4e-27	0.19	1.00		QCSR ZINC FINGER PEPTIDE;	COMPLEX (ZINC FINGER/DNA)

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fsl Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1546	1alh	A	161	249	8.5e-27	0.26	1.00		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1546	1alh	A	162	250	3e-28	0.16	0.88		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1546	1alh	A	199	277	1.5e-37	0.48	1.00		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1546	1alh	A	1	64	5.1e-22	0.31	0.80		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1546	1alh	A	281	361	3.4e-30	0.22	1.00		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1546	1alh	A	309	391	3.4e-30			80.58	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1546	1mey	C	101	185	1.5e-14	0.01	0.23		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1546	1mey	C	11	92	1e-46	0.48	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fa Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1546	1mey	C	123	249	6e-25	-0.12	0.49		PROTEIN; CHAIN: C, F, G;	INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1546	1mey	C	130	221	1.5e-39	-0.10	0.48		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1546	1mey	C	160	249	5.1e-47	0.09	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1546	1mey	C	188	277	1.7e-47	0.57	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1546	1mey	C	1	64	5.1e-34	0.26	0.95		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1546	1mey	C	224	305	1e-49	0.81	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1546	1mey	C	224	306	1e-49			105.23	DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1546	1mey	C	252	333	1.2e-49	0.59	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1546	1mey	C	280	361	3.4e-49	0.38	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1546	1mey	C	308	389	1.2e-49	0.37	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1546	1mey	C	336	411	3.4e-44	0.26	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1546	1uf6	A	132	291	1.4e-31	0.03	0.46		TFIIIA; CHAIN: A, D, 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1546	1uf6	A	196	359	1.5e-37			117.50	TFIIIA; CHAIN: A, D, 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION)

SEQ ID NO:	PDB ID	CHAIN ID	STAR T-AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1546	1ub6	A	199	342	1.5e-37	0.41	1.00		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION (TRANSCRIPTION) COMPLEX (TRANSCRIPTION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1546	1ub6	A	253	403	1.5e-37	0.32	1.00		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION (TRANSCRIPTION) COMPLEX (TRANSCRIPTION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1546	1ub6	A	309	410	1.7e-26	0.07	0.75		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION (TRANSCRIPTION) COMPLEX (TRANSCRIPTION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1546	1ubd	C	133	249	6.8e-31	0.20	0.96		YY1; CHAIN: C; ADENOVIRUS P5 ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION (TRANSCRIPTION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION INITIATOR ELEMENT; YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION (TRANSCRIPTION/DNA) COMPLEX (TRANSCRIPTION)
1546	1ubd	C	165	277	3e-40	0.28	0.99		YY1; CHAIN: C; ADENOVIRUS P5 ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION (TRANSCRIPTION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION INITIATOR ELEMENT; YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION (TRANSCRIPTION/DNA) COMPLEX (TRANSCRIPTION)

SEQ ID NO:	PDB ID	CHAIN ID	STAR T-AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT: YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1546	1ubd	C	168	277	5.1e-33	0.47	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1546	1ubd	C	16	119	3e-25	0.24	0.81		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1546	1ubd	C	19	150	1.7e-23	-0.28	0.16		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1546	1ubd	C	1	92	3.4e-29	-0.01	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION,

SEQ NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									CHAIN: A, B;	INITIATOR ELEMENT; YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1546	1ubd	C	201	333	7.5e-48	0.25	1.00		YY1; CHAIN: C; ADENOVIRUS P5 ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1546	1ubd	C	226	334	1.2e-50			97.53	YY1; CHAIN: C; ADENOVIRUS P5 ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1546	1ubd	C	250	362	1.2e-50	0.44	1.00		YY1; CHAIN: C; ADENOVIRUS P5 ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1546	1ubd	C	279	389	4.5e-47	0.42	1.00		YY1; CHAIN: C; ADENOVIRUS P5 ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1546	1ubd	C	288	389	1.7e-33	0.35	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION; INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1546	1ubd	C	306	417	7.5e-46	0.11	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION; INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1546	1ubd	C	316	410	8.5e-32	0.16	0.93		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION; INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1546	2dtp	A	63	122	1e-10	0.24	0.74		COMPLEX (TRANSCRIPTION REGULATION/DNA) TRAMTRACK PROTEIN (TWO ZINC-FINGER PEPTIDE) COMPLEXED WITH 2DRP 3 DNA 2DRP 4	COMPLEX (TRANSCRIPTION REGULATION/DNA)
1546	2gll	A	12	150	6e-32	0.09	0.68		ZINC FINGER PROTEIN GLI1;	COMPLEX (DNA-BINDING)

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									CHAIN: A; DNA; CHAIN: C; D;	PROTEIN/DNA FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1546	2gli	A	137	248	3.4e-26	-0.08	0.34		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C; D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1546	2gli	A	160	304	3.4e-32	0.34	0.94		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C; D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1546	2gli	A	224	363	1.2e-63			106.53	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C; D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1546	2gli	A	224	391	1.2e-63	0.35	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C; D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1546	2gli	A	260	388	3.4e-34	0.40	0.95		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C; D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1546	2gli	A	280	418	9e-45	0.13	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C; D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1546	2gli	A	288	410	6.8e-31	0.45	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C; D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1546	2gli	A	99	279	1.5e-42	0.14	0.99		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C; D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)

SEQ ID NO:	PDB ID	CITAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										BINDING PROTEIN/DNA
1547	1lfg	E	217	366	1e-53	0.78	1.00		16S RIBOSOMAL RNA; CHAIN: A; FRAGMENT OF MESSENGER RNA; CHAIN: X; 30S RIBOSOMAL PROTEIN S2; CHAIN: B; 30S RIBOSOMAL PROTEIN S3; CHAIN: C; 30S RIBOSOMAL PROTEIN S4; CHAIN: D; 30S RIBOSOMAL PROTEIN S5; CHAIN: E; 30S RIBOSOMAL PROTEIN S6; CHAIN: F; 30S RIBOSOMAL PROTEIN S7; CHAIN: G; 30S RIBOSOMAL PROTEIN S8; CHAIN: H; 30S RIBOSOMAL PROTEIN S9; CHAIN: I; 30S RIBOSOMAL PROTEIN S10; CHAIN: J; 30S RIBOSOMAL PROTEIN S11; CHAIN: K; 30S RIBOSOMAL PROTEIN S12; CHAIN: L; 30S RIBOSOMAL PROTEIN S13; CHAIN: M; 30S RIBOSOMAL PROTEIN S14; CHAIN: N; 30S RIBOSOMAL PROTEIN S15; CHAIN: O; 30S RIBOSOMAL PROTEIN S16; CHAIN: P; 30S RIBOSOMAL PROTEIN S17; CHAIN: Q; 30S RIBOSOMAL PROTEIN S18; CHAIN: R; 30S RIBOSOMAL PROTEIN S19; CHAIN: S; 30S RIBOSOMAL PROTEIN S20; CHAIN: T; 30S RIBOSOMAL PROTEIN THX; CHAIN: V	RIBOSOME 30S RIBOSOMAL SUBUNIT, RIBOSOME, ANTIBIOTIC, STREPTOMYCIN, 2 SPECTINOMYCIN, PAROMOMYCIN

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fst Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1547	1p4p		211	357	1e-56			64.28	RIBOSOMAL PROTEIN S5 (PROKARYOTIC) IPK3 3	
1547	1p4p		217	357	1e-56	0.53	1.00		RIBOSOMAL PROTEIN S5 (PROKARYOTIC) IPK3 3	
1549	1ej	A	119	219	0.0045	0.31	0.11		TRANSCRIPTIONAL REPRESSOR TUP1; CHAIN: A, B, C;	TRANSCRIPTION INHIBITOR BETA-PROPELLER
1553	1mev	C	172	251	5.1e-29	0.02	-0.20		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1553	1mev	C	77	169	5.1e-33	-0.41	0.09		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1553	1mev	G	77	104	1.7e-07	-0.05	0.18		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1553	1ap2		173	203	1.7e-10	0.21	-0.20		SP1F2; CHAIN: NULL;	ZINC FINGER TRANSCRIPTION FACTOR SP1; ZINC FINGER, TRANSCRIPTION ACTIVATION, SP1
1553	1ap2		78	108	8.5e-09	0.05	-0.13		SP1F2; CHAIN: NULL;	ZINC FINGER TRANSCRIPTION FACTOR SP1; ZINC FINGER, TRANSCRIPTION ACTIVATION, SP1
1553	1af3	A	69	130	1.7e-15	-0.63	0.07		TRANSCRIPTION FACTOR IIIA; CHAIN: A; 5S RNA GENE;	COMPLEX (TRANSCRIPTION REGULATION/DNA) TFIID; 5S

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									CHAIN: E, F;	GENE: NMR, TFIIB, PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA 2 GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCRIPTION REGULATION/DNA)
1553	1ubd	C	49	130	1.4e-15	-0.83	0.24		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1553	1zld		78	104	5.1e-06	-0.36	0.00		SWI5; CHAIN: NULL;	ZINC FINGER DNA BINDING DOMAIN DNA BINDING MOTIF, ZINC FINGER DNA BINDING DOMAIN
1553	2dnp	A	74	130	1.7e-06	0.04	0.36		COMPLEX (TRANSCRIPTION REGULATION/DNA) TRAMTRACK PROTEIN (TWO ZINC-FINGER PEPTIDE) COMPLEXED WITH ZDRP 3 DNA ZDRP 4	
1553	2gli	A	52	201	3.4e-41	-0.30	0.03		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1553	2gli	A	79	229	3.4e-41			54.61	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1554	1f8l	A	8	47	4.5e-07	-0.10	0.41		CYCLIN A/CDK2-ASSOCIATED	LIGASE SKP2 P-BOX; SKP1; SKP1,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									P19; CHAIN: A, C; CYCLIN AC/DK2-ASSOCIATED P45; CHAIN: B, D;	SCP2, F-BOX, LRR, LEUCINE-RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE
1558	1jkw		1	66	3e-11	-0.49	0.24		CYCLIN H; CHAIN: NULL;	CELL DIVISION CYCLIN H (RECOMBINANT); CYCLIN, CELL CYCLE, CELL DIVISION, NUCLEAR PROTEIN
1558	1qmq	B	5	62	1.5e-09	-0.36	0.28		CELL DIVISION PROTEIN KINASE 2; CHAIN: A, C; G2/MITOTIC-SPECIFIC CYCLIN A; CHAIN: B, D; SUBSTRATE PEPTIDE; CHAIN: E, F;	COMPLEX (PROTEIN KINASE/CYCLIN) CYCLIN-DEPENDENT KINASE-2, CDK2, P33 PROTEIN KINASE; CCNA, CCN1; COMPLEX (PROTEIN KINASE/CYCLIN), CYCLIN, CDK, 2 PHOSPHORYLATION, SUBSTRATE COMPLEX
1559	1alp	A	122	541	0	0.02	0.78		ELONGATION FACTOR TU; CHAIN: A, B, E, F; ELONGATION FACTOR TS; CHAIN: C, D, G, H;	COMPLEX OF TWO ELONGATION FACTORS EF-TU; EF-TS; ELONGATION FACTOR, NUCLEOTIDE EXCHANGE, GTP-BINDING, 2 COMPLEX OF TWO ELONGATION FACTORS
1559	1alp	A	165	542	0			134.70	ELONGATION FACTOR TU; CHAIN: A, B, E, F; ELONGATION FACTOR TS; CHAIN: C, D, G, H;	COMPLEX OF TWO ELONGATION FACTORS EF-TU; EF-TS; ELONGATION FACTOR, NUCLEOTIDE EXCHANGE, GTP-BINDING, 2 COMPLEX OF TWO ELONGATION FACTORS
1559	1d2e	A	122	548	0	0.41	1.00		ELONGATION FACTOR TU (EF-TU); CHAIN: A, B, C, D	RNA BINDING PROTEIN G-PROTEIN, BETA-BARREL
1559	1d2e	A	124	552	0			131.00	ELONGATION FACTOR TU (EF-TU); CHAIN: A, B, C, D	RNA BINDING PROTEIN G-PROTEIN, BETA-BARREL
1559	1edc	A	121	541	0	0.47	1.00		ELONGATION FACTOR;	RNA BINDING PROTEIN EF-TU;

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1559	1ef6	A	137	542	0			129.64	CHAIN: A, B; ELONGATION FACTOR; CHAIN: A, B;	TRANSPORT AND PROTECTION PROTEIN, RNA BINDING PROTEIN RNA BINDING PROTEIN IETU; TRANSPORT AND PROTECTION PROTEIN, RNA BINDING PROTEIN COMPLEX (TWO ELONGATION FACTORS) ELONGATION FACTOR FOR TRANSFER, HEAT UNSTABLE, ELONGATION FACTOR FOR TRANSFER, HEAT STABLE, ELONGATION FACTOR, COMPLEX (TWO ELONGATION FACTORS)
1559	1etu	A	122	541	0	-0.05	0.86		ELONGATION FACTOR TU; CHAIN: A, C; ELONGATION FACTOR TS; CHAIN: B, D;	COMPLEX (TWO ELONGATION FACTORS) ELONGATION FACTOR FOR TRANSFER, HEAT UNSTABLE, ELONGATION FACTOR, COMPLEX (TWO ELONGATION FACTORS)
1559	1etu	A	172	542	0			115.68	ELONGATION FACTOR TU; CHAIN: A, C; ELONGATION FACTOR TS; CHAIN: B, D;	COMPLEX (TWO ELONGATION FACTORS) ELONGATION FACTOR FOR TRANSFER, HEAT UNSTABLE, ELONGATION FACTOR FOR TRANSFER, HEAT STABLE, ELONGATION FACTOR, COMPLEX (TWO ELONGATION FACTORS)
1559	1ega	A	126	368	1.5e-13	0.05	0.13		GTP-BINDING PROTEIN ERA; CHAIN: A, B;	HYDROLASE ERA, GTPASE, RNA-BINDING, RAS-LIKE, HYDROLASE
1559	1etu		118	345	8.5e-67	0.18	0.45		TRANSPORT AND PROTECTION PROTEIN ELONGATION FACTOR TU (DOMAIN D) - *GUANOSINE DIPHOSPHATE IETU 4 COMPLEX IETU 5	
1559	1exm	A	117	541	0	0.29	1.00		ELONGATION FACTOR TU (EF-TU); CHAIN: A;	TRANSLATION EF-TU; GTPASE, MOLECULAR SWITCH, TRNA, RIBOSOME, Q-BETA REPLICASE, 2 CHAPERONE, DISULFIDE ISOMERASE
1559	1f60	A	120	542	0	0.31	1.00		ELONGATION FACTOR IEEF1A; CHAIN: A; ELONGATION	TRANSLATION PROTEIN-PROTEIN COMPLEX

SEQ NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1359	1fmm	A	319	439	1.7e-05	-0.15	0.00		FACTOR BEF1BA; CHAIN: B; ELONGATION FACTOR G; CHAIN: A;	TRANSLATION EF-G; BENT CONFORMATION, VISIBLE DOMAIN III, MUTATION HIS573ALA
1359	1g7s	A	123	553	8.5e-62	0.03	0.28		TRANSLATION INITIATION FACTOR IF2EF3B; CHAIN: A;	TRANSLATION TRANSLATIONAL GTPASE
1361	1al7		19	165	4.5e-09	0.08	0.07		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	HYDROLASE TETRATRICPEPTIDE, TRP- HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE
1361	1al7		2	105	1.2e-06	-0.01	0.83		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	HYDROLASE TETRATRICPEPTIDE, TRP- HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE
1361	1elr	A	19	111	1.3e-08	0.01	0.70		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
1361	1elr	A	316	401	0.0012	-0.46	0.03		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
1361	1elr	A	462	558	0.003	-0.07	0.10		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
1361	1elr	A	54	119	0.0003	0.36	0.41		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
1361	1elr	A	63	165	0.0001	-0.02	0.05		TPR2A-DOMAIN OF HOP;	CHAPERONE HOP, TPR-DOMAIN, BINDING

Seq ID NO:	PDB ID	CHAIN N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
1561	1eiw	A	19	119	7.5e-08	0.38	0.98		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
1561	1eiw	A	25	123	5.1e-06	0.26	0.71		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
1561	1eiw	A	2	97	4.5e-07	0.31	0.95		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
1561	1eiw	A	382	472	0.00034	-0.68	0.19		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
1561	1eiw	A	458	537	1.7e-05	0.41	0.12		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
1561	1fch	A	17	252	1.3e-13	0.25	0.65		PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTISI-CONTAINING PEPTIDE; CHAIN: C, D;	SIGNALING PROTEIN PEROXISOMAL RECEPTOR 1, PTISI-BP, PEROXIN-5, PTISI PROTEIN-PEPTIDE COMPLEX, TETRATRICOPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT
1561	1fch	A	2	119	1.2e-10	0.34	0.31		PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTISI-CONTAINING PEPTIDE; CHAIN: C, D;	SIGNALING PROTEIN PEROXISOMAL RECEPTOR 1, PTISI-BP, PEROXIN-5, PTISI PROTEIN-PEPTIDE COMPLEX, TETRATRICOPEPTIDE REPEAT, TPR,

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast	Verify score	PMF score	SIQFOL D score	Compound	PDB annotation
1561	1fch	A	318	363	3.4e-10	0.05	0.03		PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: C, D;	2 HELICAL REPEAT SIGNALING PROTEIN PEROXISOMAL RECEPTOR 1, PTS1-BP, PEROXIN-5, PTS1 PROTEIN-PEPTIDE COMPLEX, TETRATRICOPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT
1561	1fch	A	31	286	1.4e-11	0.10	0.48		PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: C, D;	SIGNALING PROTEIN PEROXISOMAL RECEPTOR 1, PTS1-BP, PEROXIN-5, PTS1 PROTEIN-PEPTIDE COMPLEX, TETRATRICOPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT
1563	1aw1	A	41	242	1.4e-07			68.91	APOLIPOPROTEIN A-4; CHAIN: A, B, C, D;	LIPID TRANSPORT APO A-4; LIPOPROTEIN, LIPID TRANSPORT, CHOLESTEROL METABOLISM, 2 A THEROSCLEROSIS, HDL, LCAT-ACTIVATION
1563	1cum	A	19	233	1.5e-10			68.37	ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1563	1cm	A	61	269	1.5e-10	0.04	0.03		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1563	1dn1	B	18	254	1.5e-13	-0.33	0.10		SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1A; CHAIN: B;	ENDOCYTOSIS/EXOCYTOSIS NSEC; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT
1563	1ez3	A	5	128	1.5e-07	0.19	0.00		SYNTAXIN-1A; CHAIN: A, B, C;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1563	1qpe	A	2	283	1.2e-09			66.08	VESICULAR TRANSPORT PROTEIN SEC17; CHAIN: A;	KDA PROTEIN, P35A, THREE HELIX BUNDLE PROTEIN TRANSPORT HELIX-TURN-HELIX TPR-LIKE REPEAT, PROTEIN TRANSPORT CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL, CONTRACTILE PROTEIN CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL, CONTRACTILE PROTEIN
1563	1quu	A	22	291	4.5e-17			71.18	HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	
1563	1quu	A	5	246	4.5e-17	0.01	-0.06		HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	
1563	1sig		92	287	1.2e-06	0.09	0.12		RNA POLYMERASE PRIMARY SIGMA FACTOR; CHAIN: NULL;	TRANSCRIPTION REGULATION SIGMA70: RNA POLYMERASE SIGMA FACTOR, TRANSCRIPTION REGULATION
1565	1a4y	A	11	143	1e-13	0.06	0.00		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPTOPE MAPPING, LEUCINE-RICH 3 REPEATS
1565	1a4y	A	3	176	1.5e-13	0.50	0.62		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPTOPE MAPPING, LEUCINE-RICH 3 REPEATS
1565	1f61	B	43	133	6.8e-09	0.04	-0.05		NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP/RBD OR RRM) AND LEUCINE-RICH REPEAT 2 (LRR)
1565	1f9v	A	3	140	3.4e-15	0.06	0.01		SKP2; CHAIN: A, C, E, G, I, K, M, O; SKP1; CHAIN: B, D, F, H, J, L;	LIGASE CYCLIN ACDK2-ASSOCIATED PROTEIN P45; CYCLIN

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									N, P;	A/CDK2-ASSOCIATED PROTEIN P19; SKP1, SKP2, F-BOX, LRR, LEUCINE-RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE
1565	1f9v	A	3	174	3e-17	0.74	0.99		SKP2; CHAIN: A, C, E, G, I, K, M, Q; SKP1; CHAIN: B, D, F, H, J, L, N, P;	LIGASE CYCLIN A/CDK2-ASSOCIATED PROTEIN P45; CYCLIN A/CDK2-ASSOCIATED PROTEIN P19; SKP1, SKP2, F-BOX, LRR, LEUCINE-RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE
1565	1f62	A	3	140	3.4e-15	0.23	0.07		SKP2; CHAIN: A, C; SKP1; CHAIN: B, D;	LIGASE CYCLIN A/CDK2-ASSOCIATED P45; CYCLIN A/CDK2-ASSOCIATED P19; SKP1, SKP2, F-BOX, LRR, LEUCINE-RICH REPEATS, SCF, 2 UBIQUITIN, E3, UBIQUITIN PROTEIN LIGASE
1565	2bhh		11	143	1.5e-12	0.01	0.03		RIBONUCLEASE INHIBITOR; CHAIN: NULL;	ACETYLATION KINASE INHIBITOR, RIBONUCLEASE/ANGIOTENSIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS
1565	2bhh		2	176	4.5e-10	0.18	0.35		RIBONUCLEASE INHIBITOR; CHAIN: NULL;	ACETYLATION KINASE INHIBITOR, RIBONUCLEASE/ANGIOTENSIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS
1567	2c1a		3	242	0	1.12	1.00		LYASE(OXO-ACID) CARBONIC ANHYDRASE II (E.C.4.2.1.1) (50 mM TRIS, 2CBA 3.3 M, AMMONIUM SULFATE, PH 7.8) 2CBA 4	
1567	2c1a		3	242	0			403.66	LYASE(OXO-ACID) CARBONIC ANHYDRASE II (E.C.4.2.1.1) (50 mM TRIS, 2CBA 3.3 M, AMMONIUM SULFATE, PH 7.8)	